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DEFINITION H.sapiens mRNA for IL13 receptor.
ACCESSION X95302
VERSION 91483349
KEYWORDS X95302.1 GI:1483349
SOURCE IL13R gene; Interleukin-13 receptor.
ORGANISM human.
REFERENCE 1.
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1298)
Caput, D., Laurent, P., Kaghad, M., Lelias, J.M., Lefort, S., Vita, N.
and Ferrara, P.
TITLE Cloning and characterization of a specific interleukin (IL)-13
binding protein structurally related to the IL-5 receptor alpha
chain
JOURNAL J. Biol. Chem. 271 (28), 16921-16926 (1996)
REFERENCE 96279273
AUTHORS Caput, D.
TITLE Direct Submission
JOURNAL Submitted (24-JAN-1996) D. Caput, SANOFI RECHERCHE, BP 137, F-
31676 LABEGE CEDEX, FRANCE
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DEFINITION	H.sapiens mRNA for IL-13 receptor.
ACCESSION	U08768
NID	G1877211
VERSION	Y08768.1 GI:1877211
KEYWORDS	IL-13 receptor.
SOURCE	human.
ORGANISM	Homo sapiens.
	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
	Primates; Catarrhini; Hominoidea; Homo.

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TITLE Henderson, S.L., O'Hara, R.M., Turner, K.J., Wood, C.R. and Collins, M.
JOURNAL Identification of a third chain for the murine IL-13 receptor
REFERENCE 2 (bases 1 to 1382)
AUTHORS Whitters, M.J., Donaldson, D.D., Fitz, L., Neben, T., Finerly, H. and Collins, M.
TITLE Direct Submission
JOURNAL Submitted (16-SEP-1996) Molecular Immunology, Genetics Institute,
87 Cambridge Park Dr., Cambridge, MA 02140, USA

FEATURES

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QY 902 gttaaaccttgcgcgcagctcagttgaaatatcttacttcttactcggagagattcatgt 961
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DB 850 GAAATTAAGCTGAATGAGCATACCTTTG-----GGACCTATTCCACAGAGTGT 900
QY 1022 ttgattatgaattgagatcagagaatgatactaccgcaagaatgtaggaatttgg 1081
DB 901 TTGATTATGAATTAATGATCAAGAGATGATTAATCACTACC-----TTGG 943
QY 1082 tgactgtcagctgtgaaatgaacacatcaccttgaacacaaacaaatgaaccgaataa 1141
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DB 1000 -----CAATTAATGCTTTGTAGTAGAAGCAAGTGAATTTATTTGCTCA 1044
QY 1202 gatgaaggaatttggcacaagaatcaagtagtagtgagtgagtgatataaactgtcggag 1261
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QY 1262 gtgaagacctatcgaaagaacttctgtagtgcgtgagcttcttctgctaccatttgg 1321
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QY 1322 ttcatcttaataattgattatattgttaacggtctcgtcttagtgaattgttcgtaagca 1381
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QY 1442 ttccatacaagagatgatttgatcacaagtttccagtcacatgycacaatgttcaat 1501
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RESULT 6
T81219 181219 1525 bp DNA PAT 10-JUN-1998
LOCUS

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DEFINITION      Sequence 1 from patent US 5710023.
ACCESSION       181219
NID             63209509
VERSION         181219.1
KEYWORDS        GI:3209505
SOURCE          Unknown.
ORGANISM        Unknown.
REFERENCE       1 (bases 1 to 1525)
AUTHORS        Collins, M., Donaldson, D., Fitz, L., Neben, T., Whitters, M. and
               Wood, C.
TITLE          IL-13 cytokine receptor chain
JOURNAL        Patent: US 5710023-A 1 20-JAN-1998;
FEATURES        Location/Qualifiers
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               1..1525
               /organism="unknown"
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Best Local Similarity 63.9%; Pred. NO. 2.8e-41;
Matches 681; Conservative 0; Mismatches 201; Indels 183; Gaps 14;
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QY 272 gaagagatgcagctgagatgaatgaactaaatccgaatctgtagtgaataacatga 331
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DB 424 --AAGGCTGTACACTAGAAATATGCTTAAATACCGAAATGTTGATAGCAGACCTGA 481
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QY 512 ataccacacagaagaatccagaactaaagtccaagtaagtttggtagaagatg 571
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DEFINITION    Mus musculus IL-13 receptor alpha 2 mRNA, complete cds.
ACCESSION     U65747
NID           93483093
VERSION       965747.1
KEYWORDS      GI:3483093
SOURCE        house mouse.
ORGANISM      Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
               Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 1567)
AUTHORS       Donaldson, D.D., Whitters, M.T., Fitz, L., Neben, T.Y., Finerly, H.,
               Henderson, S.L., O'Hara, R.M., Turner, K.J., Wood, C.R. and
               Collins, M.
TITLE         The murine IL-13 receptor alpha 2: molecular cloning,
               characterization, and comparison with murine IL-13 receptor alpha 1
               and collagen.
JOURNAL        J. Immunol. 161 (5), 2317-2324 (1998)
MEDLINE       98391042
REFERENCE     2 (bases 1 to 1567)
AUTHORS       Donaldson, D.D., Whitters, M.T., Fitz, L., Neben, T.Y., Finerly, H.,
               Henderson, S.L., O'Hara, R.M., Turner, K.J., Wood, C.R. and Collins, M.
TITLE         Direct Submission
JOURNAL        Submitted (31-JUL-1996) Molecular Immunology, Genetics Institute,
               87 Cambridge Park Dr., Cambridge, MA 02140, USA
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Db 111539 AAAAAAAAAATGGAACACAGCATCAAGAATTTATGAGAACATTCATTGTGAACTTGGCA 111480

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Db 111479 AACATGTTATTTTGAAGAGATATATGCGCTAAGAAATTTTTTAAATAATGACAACATTTGANC 111420

Oy      1015   aagggttcttgatttaagaattgagatcacagaagaatgatctaccgaagaatggagga 1074
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Oy      1075   atttggtgactgcctaacggttgaatatgaacatcaccttgaataaacacaatatgaa 1132
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RESULT 11
LOCUS     AB020862/c
DEFINITION Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepacocellular colorectal and non-small cell lung cancer , segment 5/11.
ACCESSION AB020862
VERSION    g4003382
KEYWORDS   AB020862.1 GI:4003382

SOURCE     Homo sapiens DNA.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Euthera; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (sites)
AUTHORS   Nakamura,Y. and Isumura,M.
TITLE      Homo saplens'1,210,381bp genomic DNA of 8p21.3-p22 anti-oncogene of hepacocellular colorectal and non-small cell lung cancer region published only in Database (1998) In press
JOURNAL    Submitted (30-NOV-1998) to the DDBJ/EMBL/GenBank databases. Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced Database Department: 5-3, Yonban-cho, Chiyoda-ku, Tokyo 102-0028, Japan (E-mail:mika@tokyo.jst.go.jp, Tel:81-3-5214-8491, Fax:81-3-5214-8470)
REFERENCE 2 (bases 1 to 100000)
AUTHORS   Hirakawa,M., Yamaguchi,H., Imai,K. and Shimada,J.
TITLE      Direct Submission
JOURNAL    Submitted (30-NOV-1998) to the DDBJ/EMBL/GenBank databases. Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced Database Department: 5-3, Yonban-cho, Chiyoda-ku, Tokyo 102-0028, Japan (E-mail:mika@tokyo.jst.go.jp, Tel:81-3-5214-8491, Fax:81-3-5214-8470)

COMMENT    This sequence is conducted by Japanese Foundation for Cancer Research as a JST seauencing team
            Principal Investigator: Yusuke Nakamura Ph.D.
            Phone:+81-3-5449-5372, Fax:+81-3-5449-5433, yusuke@ngc.ims.u-tokyo.ac.jp
            The sequence is submitted by:Human Genome Sequencing in ALIS project of JST
            Japan Science and Technology Corporation (JST)
            5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081 Japan
            For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive web site
            (http://www-alis.tokyo.jst.go.jp/HGS/top.html)
            or send email to webmaster@ww-alis.tokyo.jst.go.jp.

FEATURES             Location/Qualifiers
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ORIGIN
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Best Local Similarity 63.0%: Pred. No. 2.1;
Matches 68; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
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 Db 63693 GATTTAACCTCAAGTCAAACTCTTATATGGAAGATATAGTAGAT 63645

RESULT 12
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 AC006279
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 AC006279.4 GI:5919277
 HTG: HTGS_PHASE1.
 ORGANISM
 SOURCE
 ORGANISM
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 96304, USA
 On Sep 23, 1999 this sequence version replaced gi:4558576.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 16 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1
 7842 8041: contig of 7841 bp in length
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 67973 142824: contig of 74852 bp in length
 142825 143024: gap of unknown length
 143025 147294: contig of 4270 bp in length
 147295 147494: gap of unknown length
 147495 153406: contig of 5312 bp in length
 153407 161784: contig of 8178 bp in length
 161785 161984: gap of unknown length
 161985 163895: contig of 1911 bp in length
 163896 164095: gap of unknown length
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 177107 177306: gap of unknown length
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/rpt_family="Alusx"
repeat_region 16489..16787
/rpt_family="Alusq"
repeat_region complement(17350..17651)
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repeat_region 18464..18556
/rpt_family="Alusq/FRAM"

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repeat_region 18705..18830
/rpt_family="MIR"
repeat_region complement(1965..19012)
/rpt_family="L2"
repeat_region 19374..19463
/rpt_family="MERSB"
repeat_region 19466..19596
/rpt_family="AlusB"
repeat_region complement(19602..19656)
/rpt_family="(TA)n"
repeat_region complement(20165..20456)
/rpt_family="AlusC"
repeat_region complement(20659..20958)
/rpt_family="Alusq"
repeat_region complement(22012..22173)
/rpt_family="MERSB"
repeat_region 23088..23369
/rpt_family="Alusq"
repeat_region 23426..23528
/rpt_family="MIR"
repeat_region complement(24025..24337)
/rpt_family="Alusq"
repeat_region complement(25579..25608)
/rpt_family="AT_rich"
repeat_region complement(26719..26883)
/rpt_family="(CAT)n"
repeat_region complement(27499..27802)
/rpt_family="Alusq"
repeat_region 27811..27879
/rpt_family="AT_rich"
repeat_region 27922..28125
/rpt_family="Alusq"
repeat_region 28162..28333
/rpt_family="FRAM"
repeat_region 28387..28421
/rpt_family="AT_rich"
repeat_region complement(30101..30540)
/rpt_family="LIM4"
repeat_region complement(30725..31020)
/rpt_family="Alusx"

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Query Match 2.8% Score 43; DB 11; Length 190482;
 Negt Local Similarity 59.3%; Pred. No. 3;
 Matches 77; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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C 1322 ttccatttataatgattatattgtaaccggtctctagagaatggtcggaagca 1381
Dh 143386 TATATATGATCCACTTATATATAGCTAAACCTGTCATATCATTCATCAAAATACCAA 143445
Q 1382 aaccuccaccocaaagattccgaattttctgtgatacatgaagaattgcatct 1441
Dh 143446 ATTCATCTCTGTAATAATATTCATGAAGTTTTCGTATGCCAGACAGACATTTGAATTA 143505

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0% 1442 ttc 1444
 111
 Dh 143506 TTC 143508

RESULT 14
 ECHRSFX6 2402 bp DNA ECT 12-MAY-1995
 LACUS Escherichia coli extended core protein Rhes and ORF f202 genes,
 DEFINTIN partial cds, and unidentified ORF, complete cds.
 ACCESSION U5127
 NID 9563992
 VERSION U5127.1 GI:563992
 KEYWORDS 6 of 6
 SOURCE Escherichia coli.
 ORGANISM Escherichia coli.
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Escherichia.
 REFERENCE 1 (bases 1 to 2402)

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Result No.	Score	Query Match	Length	DB	ID	Description
1	1539	100.0	1539	1	T85826	Human Interleukin
2	857	55.7	1298	1	T86646	Human Interleukin
3	851	55.3	1269	1	T95214	CDNA encoding the
4	840	54.6	1389	1	T96782	Human zeytor2 cyto
5	830	53.9	1288	1	V04075	Human cytokine/pep
6	830	53.9	1288	1	V02305	Homo sapiens CDNA
7	830	53.9	1288	1	V04131	Human Hk-1 recepti
8	727.2	47.3	1167	1	T96783	Human zeytor2 cyto
9	624	40.5	1126	1	T96784	Celebs macaque zc
10	595	38.7	1079	1	V22701	Construct containi
11	595	38.7	947	1	V22702	Mature interleukin
12	287	18.6	456	1	V87956	EST clone CS520. N
13	242.4	15.8	465	1	V22698	Interleukin-13 bli
14	237.4	15.4	465	1	V22698	CDNA encoding the
15	221.6	14.4	473	1	T95213	Interleukin-13 bli
16	36	2.3	2398	1	V06554	Outer membrane 14
17	36	2.3	1618	1	V74914	Staphylococcus au
18	35.8	2.3	110000	1	V21309_14	Continuation (15 c
19	35.8	2.3	272	1	V90526	EST clone BK384. N
20	35.6	2.3	1721	1	X07566	Homo sapiens fetal
21	35	2.3	110000	1	V21209_11	Continuation (12 c
22	35	2.3	11624	1	V52850	Human Eyt gene cD
23	34.6	2.2	1002	1	T68933	Bovine PIT-1 exon
24	34.6	2.2	6810	1	X20267	Borrelia burgdorfe
25	34	2.2	7459	1	N91312	PCPII plasmid. Sym
26	34	2.2	7502	1	Q27429	PCPII plasmid
27	34	2.2	110000	1	T58840_4	Continuation (5 o
28	33.8	2.2	110000	1	V21209_09	Continuation (10 c
29	33.8	2.2	3704	1	V54590	Human secretory pr
30	33.8	2.2	812	1	X39990	Prostate cancer as
31	33.6	2.2	6124	1	Q03568	Sequence encoding
32	33.4	2.2	10357	1	V52324	Streptococcus pneu
33	33.4	2.2	1532	1	X00641	Human secreted pre
34	33	2.1	110000	1	V21309_06	Continuation (7 o
35	32.8	2.1	8805	1	X13072	Enterococcus faeco
36	32.6	2.1	237326	1	V57803	Hereditary haemoch
37	32.6	2.1	6254	1	V74715	Staphylococcus au
38	32.6	2.1	45546	1	X23520	Human kidney amin
39	32.4	2.1	1285	1	Q26097	MIG-1. New monoki

18] *cgagata.y-ggat*

QY	1321	ggttattcttataattagttatatttgtaaacgggtctgattgaattgctgaaacc	1380
DV	1321	gatttatcttattatttattgtattatttttaaccgcgctgcgttgatgtgaattgctgaacc <td>1380</td>	1380
QY	1381	aaacaccaccacaaataatgatccaaagattttctcttgataatgaagaatttgatc <td>1440</td>	1440
DB	1381	aaacaccttaccacaaatnagattccaaattttttcttgatnactaagaagatttgatc <td>1440</td>	1440
QY	1441	tttcatactcaagagacatggtattgactcaacagtttccagtcattgcccgaattgca <td>1500</td>	1500
DB	1441	tttccatattcaagagacatggtattgactcaacagtttccagtcattgcccgaattgca <td>1500</td>	1500
QY	1501	tatgagctcacaataatgaattttttcttgcaagtttg <td>1539</td>	1539
DB	1501	tatgagctcacaataatgaattttttcttgcaagtttg <td>1539</td>	1539
RESULT	2		
ID	186464	standard; DNA; 1298 bp.	
AC	186464		
DT	22-JUN-1998	(first entry)	
DE	Human interleukin-13 beta receptor DNA.		
KE	Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13; ss.		
OS	Homo sapiens.		
FE	Key	Location/Qualifiers	
FT	CDS	53..1195	
FT		/tag= a	
FT		/product= IL-13_beta_receptor	
PD	MO9700926-A1		
PE	12-JUN-1997		
PR	07-NOV-1996; F01756.		
PR	06-DEC-1995; FR-014424.		
PA	(SNFI) SANOFI SA.		
DR	Caput D, Ferrara P, Laurent P, Vita N;		
DR	MP1: 97-319773/29.		
DR	P-PSDB: W24972.		
PT	New purified human interleukin-13 receptors - and related nucleic		
PT	acids, useful for diagnosis and treatment of inflammation, allergy,		
PT	etc		
PS	Claim 6; Figure 2a; 83pp; French		
CC	This sequence encodes human interleukin-13 (IL-13) beta receptor. The		
CC	invention relates to new purified peptides comprising 380 or 427 amino		
CC	acid sequences, which are receptors for interleukin-13 (IL-13); the 380		
CC	and 427aa proteins are designated IL-13R beta and alpha respectively.		
CC	The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low		
CC	affinity, but acquires high affinity when associated with the IL-4		
CC	receptor. Nucleic acids encoding IL-13R beta and alpha are used as		
CC	diagnostic probes to identify aberrant synthesis or genetic anomalies		
CC	such as loss of heterozygosity and rearrangements, or chromosomal		
CC	anomalies. They are also used for production of recombinant IL-13R beta		
CC	and alpha which can be used as IL-13 antagonists, specifically to		
CC	regulate IL-13-induced responses for treatment of inflammation and		
CC	allergy. IL-13 receptors are also useful as antisense molecules for gene		
CC	therapy (blocking synthesis of IL-13R). Antibodies are used (in standard		
CC	immunoassays) to diagnose diseases associated with abnormal expression,		
CC	overproduction of IL-13 receptors. When coupled to a toxin also for treatment of		
CC	used to identify ligands and modulators of IL-13R at the surface are		
CC	is encoded by the nucleic acid sequence shown in Figure 2a in the		
CC	specification (T86464), which is not the same as that shown in the		
CC	sequence listing (T85826).		
SC	Sequence 1298 BP: 407 A; 231 C; 266 G; 394 T;		
Query Match	55.7%; Score 857; DB 1; Length 1298;		
Best Local Similarity	84.3%; Pred. No. 4,5e-224;		
Mismatches	0; Conservative 0; Mismatches 0; Indels 241; Gaps 20;		

QY	61	atctgtttgctgctatcgagctatatactcttcgataagaacaacttgctg	120
DB	59	-TTGCTTGGCTGGCTATGCGATGCTTATATACCTTCTTGATATAGACAAACTTTGGCTG	117
QY	121	tacaagctttgcactcatcttcagaacacgagataaagaattaaccttcctcaggattc	180
DB	118	T-----ACTTCATCTTCAGACACCGGATATAAAGTTAAACCCCTCCAGATT	165
QY	181	tgagatagtgattatgaagaagaccggatcttgatctcatttgtaagggaa	240
DB	166	TGAGATATGTGAT-----CCGGATACTTATGGTATCTCATTTGCAATGGCA	214
QY	241	cccccactgctcctgatacatttgctgtttgtaagaagatgacagtggatatgacta	300
DB	215	CCCCACTGCTCTCGATCATTTT-----AAGATATGCACAGTGAATATGACTA	265
QY	301	aaataaccggaacattggttagtgaacaatggaagcctagtgtgagagttacacattact	360
DB	266	AAATATCGGAAACATTTGTATGTGAATACTGAAAG-----ACCATCTATTACT	310
QY	361	aagatcttacctacaagaatgggtttgatctcttaacaaggacatgaaatataagaaggc	420
DB	311	AAGATATTACATTACAAAGATGGGTTTGATCTTTACAAAGGCATTCGA-----GC	360
QY	421	gaagatcacacgccttttaccatgycaatgacacaaatgatalcaagaattcaaatgacaa	480
DB	361	GAAATATACACACGCTTTTACCATGCAATGCACAAATGATCATGAAGTCAAAAGTTCC--	419
QY	481	ttgttagagtagtggacagaactactatattgatatccacaagaagaattccagaacaa	540
DB	419	-----TGGCACAATACTACTTATTTGGATATATCCACAAAGGATATCCGAATCTAA	468
QY	541	agttcaggaatgaagtttggtagaatyatgycgataltaacaattgycaaattact	600
DB	469	AGTTCAGGAT-----ATGATTTGCGTATATTCAATTTGGCATATTTACT	513
QY	601	ctgtctcttggaaaccctggcaltaggttacaattatgcttggtaactcttgataccaattac	660
DB	514	CTGTCTCTTGGAAACCTTGCGATAGT-----GTACTCTTGTATCCAAATTAC	559
QY	661	aacttggtttacctgtaatggagcctggatcatgcatataatatattggaacaagtgtg	720
DB	560	AACCTGTTTACTGATAGGCGCTTGATCATATGCTT-----ACAGTGTG	605
QY	721	ttgatcacatcaagcctgatalgacaataataagatgcatgcatcttcctatttggcaata	780
DB	606	TTGATTTACATCAAGCGTGATGGACAAATATATAGATGCAGATTTCCCTATTG-----	659
QY	781	agagagcgtgagcatcagaactataaagtttctatatatttggttaatgatatcatcaag	840
DB	659	-----GAGGATATGACTATTAAGATTTCTATATTGTGTATATGATCATCATCAG	709
QY	841	aacaagccttaaatatcatcaagaagaatcagatccagttatctactcttcagcttcaaatat	900
DB	710	AACAAGCT-----ATCAGATCCGATTATTTACACTTTTCAGCTTCAAAATAT	756
QY	901	agttaaacctttgcgcgcagtcagttggaataatcttacttcttaactcgggagaattcag	960
DB	757	AGTTAAACCTTTGGCCGCACATC-----TATCTTACTTTTACTCGGAGATGTTATAG	807
QY	961	tgaattaaagctgaatcggagcatalactcttggttagcggtgagacctatccagaaagt	1020
DB	808	TGAATTTAAGCTGAATGGAGCATACCTTTG-----GAACTATTCCACGCAAGTG	858
QY	1021	ttttgattatgaatltgatacagagaagatgatalactacccaagaacatgtaggaatttg	1080
DB	859	TTTTGATTATGAATTTAGATTCAGAGAAGATGATATCTACC-----TTG	901
QY	1081	gtgagctctcagttgaaatgaaatcaccctctgaaacacaaatgaaacccgata	1140
DB	902	GTGCTCTCAAGTTGAAATGAAACCTACCTTATAAACAACAATGAATCAACCGCA--	959

Cy	1141	atagagctcttagaggaatattgctctcttgagaagaacgaagtgatattatctgc	1200
Dh	959	-----CAATTATGCTTTGTAGTACGAAACAAAGTGATATTATTGCTC	10022
Q3	1201	agatcaaggaattctgggcaaaagaatcaagtagtagtgagtgagtgataaacaatgctgggaa	1260
D8	1003	AGATGACGGAAATTGG-----AGGATGTGAGTGATTAACAAAGCTGGGAA	1048
QY	1261	ggtaagaacctatctgaagaagaactttgcttagtagctggatctggtttctggctaccatttg	13202
D3	1049	GGGGAAGACGATGAGGAAGAAACTTTGCTA-----CGTTTCGGCGTACCATTTG	1097
QY	1321	gttcaccttaattatgattatattggttaaccggctctgcttgatgaatgctggcgaagcc	1380
Ed	1095	GTTTCATCTTATATTAGTTATATTGTTACCGGCTGCTT-----TTGCGTAAACC	1149
QY	1381	aacacattaccacaazaatgatcttcagaatctttctgtgatacatgaagaagatctgac	1440
F3	1150	AAACACGTACCCAAAATATGATTCAGAAATTTTCTGTATACATGAAG-----C	1199
QY	1441	ttccatacataagagacatggtatctgaactacaagttccagtcacatggccaagtctaa	1500
Ed	1200	TTTCCATATCAAGAGACATGTGATTTACCTCAACAGTTTCCATCATGCGCAAAATGTTCA	1259
QY	1501	taigaatcataaanaactgaattctctggcaattg	1539
Ed	1260	TATGAGTCTCATTAACCTGAATTTTCTTGGCAATGTTG	1298

RESULT	3	
TS5214		
TS5214	standard: cDNA: 1369 BP.	
AC	TS5214	
BT	27-MAR-1998 (first entry)	
DE	cDNA encoding the human IL-13 binding chain of the IL-13 receptor.	
KW	Interleukin-13; IL-13; Interleukin-13 receptor binding chain; IL-13bc;	
KW	mediator; IL-13 receptor binding inhibitor; IGE-mediated condition;	
KA	allergy; asthma; immune complex disorder; ds.	
OS	Homo sapiens.	
FT	Key	Location/Qualifiers
FT	CDS	103..1245
FT		/*tag- a
FT	sig_peptide	103..177
FT		/*tag- b
FT	mat_peptide	178..1242
FT		/*tag- c
PN	W0973194F-A1.	
PD	04-SEP-1997.	
PD	28-FEB-1997: U03124.	
PK	01-MAR-1996: US-609572.	
PI	(GENY) GENETICS INST INC.	
PI	Collins M, Donaldson D, Fitz L, Neben T, Whitters M,	
PI	Wood C,	
PI	WPI: 97-418632/41.	
DR	P-PSDB: W35295.	
PT	New nucleic acid encoding interleukin-13 receptor binding chain and	
PT	transformed cells - proteins, antibodies and inhibitors, for	
PT	treating immunoglobulin E-mediated diseases, e.g. Graves disease,	
PT	and in diagnosis	
PS	Claim 1: Pages 32-33; 49pp; English.	
CC	The present sequence encodes the human interleukin-13 (IL-13) binding	
CC	chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a	
CC	mediator of the known biological activities of IL-13. The present	
CC	sequence was isolated from human testis library. Recombinant	
CC	IL-13bc proteins, and antibodies raised against them, are used to	
CC	inhibit the binding of IL-13 to its receptor. They are particularly used	
CC	to treat IGE-mediated conditions, e.g. allergy, asthma and immune complex	
CC	disorders, especially lupus, nephritis, thyroiditis and Grave's disease.	
CC	It is also used to treat immune deficiency (particularly in	
CC	hematopoietic progenitor cells), cancer etc., and to increase macrophage	
CC	activation, e.g. in vaccination. To potentiate IL-13 activity, a protein	
CC	with such activity is combined with IL-13bc and the mixture applied,	
CC	in vivo, to a cell expressing at least one chain of the IL-13 receptor	

PR 12-JUN-1996; US-017843.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PI Appelbaum ER, Hu J.
 DR WPI: 98-034974/04.
 DR P-PSDB: W41502.
 PT Human cytokine/peptide hormone receptor, HR-1 receptor - useful to
 PT increase resistance to infections in individuals with trauma and/or
 PT burns
 PS Claim 4: Page 26-27: 34pp: English
 CC This cDNA clone codes for a novel human cytokine/peptide hormone
 CC receptor, designated HR-1 receptor (see W41502). Plasmid ARG-531,
 CC comprising HR-1 receptor cDNA contained in vector Bluescript SK+,
 CC is deposited in E. coli JM101 as ATCC 98069. The clone was
 CC isolated from a human testis cDNA library. Also claimed are a
 CC polypeptide comprising amino acids 1-380 or 22-380 of the 380
 CC residue HR-1 receptor amino acid sequence, a vector comprising
 CC polypeptide, antibody against the polypeptide, an agonist to the
 CC that inhibits the activity of the polypeptide, and an antagonist
 CC protein and polynucleotides can be used for research, biological,
 CC diagnosis and (gene) therapy applications, e.g. to increase
 CC resistance to infections in individuals with trauma and/or burns,
 CC and to prevent, ameliorate, treat, diagnose and/or determine
 CC predisposition to asthma, allergic disorders or disorders of
 CC haematopoiesis induced by AIDS, aplastic anaemia, congenital or
 CC cyclic neutropenia or as a consequence of cytotoxic therapy of
 CC cancer, lymphoma, leukemia and/or bone marrow transplantation.
 SO Sequence 1288 bp; 421 A; 227 C; 252 G; 388 T;

Query Match 53.9%; Score 830; DB 1; Length 1288;
 Best Local Similarity 84.1%; Pred. No. 1e-216;
 Matches 1271; Conservative 0; Mismatches 0; Indels 241; Gaps 20;

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OY 23 ggcaatcaaggttttaactctcgagagaatggccttaattcgttcttgccatgga 82
DB 1 GGCATATCAAGGTTTAAATCTCGAGAAATGCT--TTCGTTCTTGGCATATGGA 57
OY 83 tgcctatataccttctgataagacacacatttggctgtacaagctttgcaactc 142
DB 58 TGGTATATACCTTTCGATAGACACACATTTGGCTGT-----ACCTCATCT 105
OY 143 tcaaacaccgagataaaagttaaccctccacagatttagatagatgattagaag 202
DB 106 TCAACACCCGAGATMAAGTTAACCTCTCAGAGATTAGATAGAT----- 157
OY 203 aaccggatacttaggttattctatttgaataggcaaccctcgtctcgtgacatt 262
DB 157 -CCCGATATCTTAGGTATCTATTTGCAATGCAACCCCACTGCTCTGATCATT 214
OY 263 ttgtgtgtgtaaaaggaatgacagttgaaatgaaataacgaaacatttggaag 322
DB 215 TT-----AAGGATGACAGATGGAATATGAATAAATCCGAACATTTGGTAG 265
OY 323 aaacatggaagtagttagaggttaccattcttaagaatctacatacacaagtg 382
DB 266 AACATGAGAG-----ACCATCATTACTAAGATCTACTACAAAGATG 310
OY 383 ggtttgattcttaacaaggcatgaaatagaaaggcgaagatacaacgctttaca 442
DB 311 GGTTCATCTTAACAAGGCGCATTGAA-----GCCAATATACACACGCTTTTACCA 360
OY 443 tggcaatgacaatgagatcagaagttaaaagttccaattgctagaggtggcagaagt 502
DB 361 TGGCAATGCAAAATGAGATCAGAAATCAAAATGCTC-----TGGCGAAGAACT 408
OY 503 acttattggaataccacaagaagaaatccagaactaaagttaagtttaagtttggt 562
DB 409 ACTTATTGATATCACCAAGAGATTCAGAACTAAAGTTTCAGAT----- 457
OY 563 agaagattcgttatatacaattggcaataattactctgttcttggaaacctggcata 622

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DB 457 ---ATGATTCGGATATATTACAAATTGGCAATATTACTGTTCTTGGAAACCTGGCATA 513
OY 623 gttacataatgctcgtggttaacttcttgataccaattacaactgttttactgtagag 682
DB 514 GGT-----GTACTTCTTATACCAATTAACAATCTGTTTACTGATATAGAG 559
OY 683 gtttgatcatgacttaataataatttgaaacagtggtgtgattgacataagcgtatg 742
DB 560 GCTTGATATGACAT-----ACAGTGTGTTGATTACATCAAGGCTGATG 605
OY 743 acaaatatagatgacagattccctatttggcaataaaggacagtgagcagact 802
DB 606 ACAAATATGAGATGACAGATTTCCTATTG-----GAGCATCAGACT 649
OY 803 ataagattctatatttggtaagatcatcagaagacagaagcctgaataatacaga 862
DB 650 ATAAAGATTCTATTTTGTATGATGATCATCAGAGAAACAGCT----- 697
OY 863 atcagatcagttatttcaacttctcagctcaaaatataatgtaaaccttggccagtc 922
DB 697 ATCAGATCCAGTATTTCACTTTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 756
OY 923 agtggaaatcttcttcttctcctcgtggagagttcaatgaaatgaatgaaatgagc 982
DB 757 -----TACTTACTTTTACTCGGAGAGTTCATGTGAATTAAGCTGAATGAGAGC 807
OY 983 atccttctttagcgttgagcctatccagaaggtgttggtaataatgagatc 1042
DB 808 ATACCTTTG-----GGACCTATTCACAGCAAGCTTTTGTATTAAGAAATGAGATC 858
OY 1043 agagaagatgatactaccagaaatgcatggaagaatttggtagctctacagttgaaatg 1102
DB 859 AAGAGAGATGATATAC-----TTGGTACTGCTACAGATTGAATGAAATG 901
OY 1103 aaacataccttggaaacaaacaaatgaaacccgaaataatagattttagtgaacta 1162
DB 902 AAACATACACCTTGAACCAACAAATGAACCA-----CAATTA 942
OY 1163 tgccttgaatgaagaagaagtgaataatttgcataatgacagaaatttggcagaag 1222
DB 943 TGCCTTGAATGAAGAGCAAAATATTTATTTGTCAGATGACGGAATTTG 997
OY 1223 aatcaagtagtgaatgagatataacaatgctgggaagttgaagcctatcgaaanaa 1282
DB 997 -----AGTGAATGAGATGATTAACATGCTGGAGGTGAAGACCTATCGAAGAAA 1048
OY 1283 cttagtagtgcgtggaatcgttctcgtacacatttggtttcaatcttaattagttat 1342
DB 1049 CTTTGCTA-----CGTTTCTGGCTACCATTTGTTTCATCTTAATTTAGTTAT 1097
OY 1343 attgtaacggctcgtttagtgaatgctgtaagcgaacacccatacccaaaatgatt 1402
DB 1098 ATTGTGAACGGCTGTGTT-----TTGCTGAACCAACCACTTACCAAAATGATTT 1149
OY 1403 ccagaatttctgctatatacagaagaatttgcattcttccatatacaagaagatg 1462
DB 1150 CCAGAATTTTCTGATATCATGAGA-----CTTTCATATCAAGAGCATGCT 1199
OY 1463 attgactcaacagtttcagttatggcgaatgccaatgltcaataatgagttcaatg 1522
DB 1200 ATGACTCAACAGTTTCCAGTATGCGCAATGTTCAATATGAGTCTCAATTAACCTGAA 1259
OY 1523 tttcttgcga 1534
DB 1260 TTTTCTTGGAA 1271

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RESULT 6
 IL V02295 standard; cDNA; 1288 bp.
 AC V02295;
 DT 08-JUN-1998 (first entry)
 DB Homo sapiens cDNA encoding the HR-1 receptor.


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OY 1343 atfgraaacggcttcgcttaagtgaaagtgtgcgttaagcacaacacccccaacaaatgatt 1402
DB 1098 ATTTGTAAACGGGTCTGCTT-----TTGGCGTAACCCAAACACCTCAACCAAAAAGATT 1149
OY 1403 ccagaattcttcgtgatcacatgaagaagatttgcattcttcacatacaagaacatggt 1462
DB 1150 CCAGAAATTTTCTGTGATCATGAGAA-----CTTTCATATCAAGAGACTGGT 1199
OY 1463 atgactcaacagtttcacgtcatgagcacaatggttcaataatgagttcaataacatgaat 1522
DB 1200 ATTGACTCAACAGTTTCCAGTCATGCGCCAAAGTTCCATATGAGTCTCATTAACATGAAAT 1259
OY 1523 tttttcttgcaa 1534
DB 1260 TTTTCTTTCGGA 1271

RESULT      8
T96783
ID T96783 standard; cDNA: 1167 BP.
AC T96783;
DT 30-MAR-1998 (first entry)
DE Human zcytor2 cytokine receptor cDNA.
KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
KW infertility; antagonist; contraceptive; diagnostic; therapeutic; ds.
OS Homo sapiens.
FH Key
FH CDS
FH Location/Qualifiers
FT 10..1152
FT /*tag= a
FT /product= zcytor2
FT /note= "cytokine receptor"

MO9733913-A1.
PD 18-SEP-1997.
PF 12-MAR-1997; U04043.
PR 13-MAR-1996; US-013345.
PA (ZYMO ) ZYMOGENETICS INC.
PI Baumgartner JW, Farrah TM, Foster DC, Grant FJ,
PI OHara FJ,
PI WPI: 97-470820/43.
DR P-PSDB: W36614.
PR New nucleic acid encoding testis-specific cytokine receptor - useful
PT for identification of ligands or antagonists, potentially for use as
PT male contraceptives or for infertility treatment
PS Claim 2; Page 49-51; 79pp; English.
CC This sequence encodes a novel ligand-binding receptor, Zcytor2, which
CC shares homology with cytokine receptors and was isolated from a human
CC testis cDNA library. The resulting polypeptide is a receptor for
CC cytokines (particularly interleukin-13) and is expressed on the surface
CC of testicular cells, probably being involved in spermatogenesis. It can
CC be used to detect ligands that promote proliferation and/or
CC differentiation of such cells in cultures and may also be used to treat
CC infertility. Antagonists of this receptor may be used to characterise
CC ligand-receptor interactions and as male-specific contraceptives. By
CC blocking the action of IL-13, receptor antagonists and ligand-binding
CC this receptor can also be used to modulate immune function, e.g. in
CC allergy and asthma, as a diagnostic to determine circulating levels of
CC ligand and also to isolate and purify ligands. Antibodies can be used to
CC assay circulating receptor (an abnormal level may be indicative of
CC disease such as cancer), for labelling cells that express the receptor,
CC and therapeutically as antagonists.
SQ Sequence 1167 BP; 365 A; 213 C; 233 G; 356 T;

Query Match 47.3%; Score 727.2; DB 1; Length 1167;
Best Local Similarity 83.1%; Pred. No. 9,6e+189;
Matches 1137; Conservative 0; Mismatches 3; Indels 228; Gaps 18;

OY 62 ttcggttgcgtgcatacggatgcatatataccttctgataagaacacacatttgcctgt 121
DB 16 TTCGTTTGCTTGCGATCGAGATCGATTATATACCTTCTTGATTAAGCACACATTGGCTGT 75
OY 122 acaagctttgacttcaatcttcagacacccggatataaagttaaccttcctcaagatttt 181
DB 122 acaagctttgacttcaatcttcagacacccggatataaagttaaccttcctcaagatttt

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Db	76	-----ACTCATCTTCAGACACCGAGATAAAGTTAAACCTCCTCAGGATTTT	123
Cy	182	gagagagagatataagaagaacccggataacttaagttatctctatttgcaatggcaac	241
Dc	124	GAGATATATGAT-----CCGGATACTTAAAGTTATCTATTTGGCAATGGCAAC	172
Cy	242	ccccacgtctctctgcatctttgtgtgtgaaggaaagcaagtgatgtgactaa	301
Cy	173	CCCCAGCTCTCTGATCATTTT-----AAGAAATACACAGTGAATATGACATA	223
Cy	302	aatccgaacatctgtgagtgaaacatgtaggctagttgaggtttaccatcattacta	361
Db	224	AATACCAAAATGTGATGAGAAACATGAG-----ACCATCATTTACTA	268
Cy	362	agatctacattacaagaatggtgtttgatcttaacaaggagcttgaaatatagaaggcg	421
Db	269	AGTACTACATTAAAGAATGAGTTTGATCTTTAACAAAGGCAATTGAA-----CGC	318
Cy	422	aagatcacaaagctttaccatgtgcaatgacacaatggatcagaagttcaagttccaat	481
Dc	359	AAGTAAACACAGCTTTTACCATGGCAATGCACAAAGATGACGAAGTTCAAGTTCC---	376
Cy	482	tgtctgagtgaggagaacactactttttgatataccacaaggaaattccagaactaa	541
Dc	376	-----TGGGAGAAATCTACTTAATGATATCCCAAGAAAGATTCCAAAACTTAA	426
Cy	542	gtctcagattaagtttttggtagaagtgatgtgataattacaaatgtgcaatttactc	601
Db	427	GTTCCAGAT-----ATGAGATTGGTATATTACAAATGGCAATATTACTC	471
Cy	602	tgctcttggaaacctgtgcataagtttcaataatgtctcggtacttcttgataccaatca	661
Dc	472	TGTTCTTGGAAACCTGGCATAGT-----GTACTCTTGATATACCAATTCA	517
Cy	562	actgttttaactgtatagaagggcttgatcatgcatcaataatatattggaacagttgt	721
Dc	518	ACTGTTTTACTGATAGAGGCGCTGGATCTTGCAAT-----ACAATGTGT	563
Cy	722	tgattacatcaaggtctgtatgacaataatagatgacagattccctatttggcaataa	781
Db	564	TGATTACATCAAGCTGATGACAAAATATAGATGCAGATTCCCTATTG-----	616
Cy	782	ggagcagtgaggctcagactataaagattctatatattgtgttaatggatcatcagaa	841
Dc	616	-----GAGGCGATCAGACTATAAAGATTCTATTTGTGTATATGATCATCAGAGA	667
Cy	842	acaagctgtaatatcaagaatcaatcacaagttatttacttcttcagcttcaaatata	901
Db	668	ACAAGCCT-----ATCAAGTCCAGTTATTTACCTTTACGTTCAAAATATA	714
Cy	902	gttaacatttgcgcgcagctggtgtggaatatatttacttcttcgcggagagttcatgt	961
Dc	715	GTTAAACCTTGCCGCCAGTC-----TACTTACTTTTACTCGGAGAGTTCACT	765
Cy	962	gaattaaqctgaaatgagcatcaccttgtgttaagcgtgagcctattccagcaaggtgt	1021
Db	766	GAAATTT/SCGAAATGGGCGCATACCTTTG-----GACCTATTTCCACAGAGGT	816
Cy	1022	ttgatatatgaattgagatcagaagaagatgatactaccggaagaacatggagaatttgg	1081
Dc	817	TTTATATTATGAATGTGATCAGAGAGATGATATAC-----TTTG	859
Cy	1082	tgaatgctcagttgaaatgaaacatacacccttgaaacacaacatgaaccggaataa	1141
Dc	860	TGATCTCTACAGTTGAAAAAGAAACATACCTTGAAAAACAACATGAAACCGCA----	916
Cy	1142	ttagagtttttagtagcaataatgtctttagtagtaagaagaatgaaatatatttgcctc	1201
Db	916	-----CATATCTCTTTAGTATAGTAAAGCAAGTAAGTAATTTATGTCTCA	960
Cy	1202	gtctcaggaatttgggcgaagaatcaagctgtgtgtgtgtgtgtataaacaatgtctggag	1261
Dc	861	GATATCGGAATTTGG-----AGTGAGGAGTATATAACATCTCTGGGAG	1006


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Db 990 ATAAACATGTTGGAGATTGAAGAACTATGAGAAAACCTTGCTA-----CT 1038
Oy 1304 ttccggctaccatttggttcacctaataatagtaatttgtaaccggtctgtag 1363
Db 1039 TTCTGTGTACCATTTGGTTTCATATATATATATATATATATATATATATATAT 1097
Oy 1364 tgaatggtcgtgaagccaacacccaccccaaatatg 1399
Db 1097 -----TTGTCTAAGAGAGACAGCTACCCGAAATG 1126

RESULT 10
ID V22701
AC V22701 standard; DNA; 1079 BP.
DE Construct containing mature Interleukin-13 binding protein gene.
KW Therapeutic; IL-13 mediated condition; allergy; asthma; diagnosis;
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1078
FT FT /*tag= a
FT FT /product= "Mature IL-13 binding protein"
FT FT /note= "No stop codon given"
PN M09810638-A1.
PR 19-MAR-1998.
PR 10-SEP-1997; AU-005374.
PR 27-FEB-1997; AU-005374.
PR 10-SEP-1996; AU-002262.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PR Hilton DJ, Nicols NA, Simpson RJ, Zhang J;
DR WPI: 98-207062/18.
DR P-PSDB: W56260.
PT New isolated Interleukin-13 binding protein - used to develop
PT products for therapy e.g. for allergic conditions such as asthma or
PT for diagnosis or detection
PS Example 14; Page 50-52; 69pp; English.
CC The IL-13 binding protein and related therapeutic molecules can be used for
CC in the antagonism of at least one IL-13 activity. They can be used for
CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.
SQ Sequence 1079 BP; 341 A; 209 C; 227 G; 302 T;

Query Match 38.7%; Score 595; DB 1; Length 1079;
Best Local Similarity 82.7%; Pred. No. 9.2e-153;
Matches 942; Conservative 0; Mismatches 0; Indels 197; Gaps 15;
Oy 152 gagataaagtaaccccccacagatttgagatagtgatataagaagaacccgat 211
Db 133 GAGATAAAGTTAACCCCTCTCAGATTGATGATGATGATGATGATGATGATGATGAT 181
Oy 212 acttaggtatctctatttgcaatgcaaccccccacagcttctctgatacttggttgt 271
Db 182 ACTTAGGTATCTCTATTGTAATGCAACCCCACTCTCTCTGATCATTTT----- 235
Oy 272 gaaaggaatgacagtggaatataaactaaataccgaacattggtatgaacatgga 331
Db 235 --AAGGAATGCACAGTGAATATGAAATGAAATACCGAATGATGATGATGATGATGATGAT 292
Oy 332 aggtctagtgtagaggtacccatctactataagaatctcatataagaatggtgtgtc 391
Db 293 AG-----ACCATCACTTACTAAGAACTCAATTAACAAAGATGGTTGATC 337
Oy 392 ttaacaaggaatgaaatataagaagcggaagatacagacgctttacacagtgcaatgc 451
Db 338 TTAACAAGGCAATGAA-----GCGAAGATACACAGCTTTTTCATGCGCAATGC 387
Oy 452 acaaatgatacagaagtccaagtccaattgtagaggtggcagaacactactattatg 511

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Db 563 A--AATGATCAGAGATTCAAGTCC-----TGGCGAAGAACTATTATGG 435
Oy 512 atcacacacaggaatccagaacctaagaattgaagtaagtgtggtagaatgat 571
Db 436 ATATCCACCAAGGAATCCAGAACTAAGTTAGAT-----ATGGAT 480
Oy 572 tgcgcatattcaattgcaatattactctgtctctggaacctggcatagttacatt 631
Db 481 TGCCTATATTTCATTTGCAATATATTACTGCTCTTGGAAACCTGGCATATGGT----- 535
Oy 632 atgtctggtactctctgataccaattacaactgttttactgtatagggcttgatc 691
Db 535 -----GTACTCTTGATACCAATTAACAATTGTTTACTGATATGAGGCGCTTGATC 586
Oy 692 atgatttaaatattttggaacagtggtgtgataataagctgataagacaatat 751
Db 587 ATGCAAT-----ACAGTGTTGATTACATCAAGGCTATGACAAATAT 632
Oy 752 aggatgcagatccctatttggaatgaagagcagtgagacacacataaagatt 811
Db 633 AGGATGCAAGATTGCCATTTG-----GAGGCATCAGACTATTAAGATT 676
Oy 812 tctatattggttaatgatacagagaacaagcctgaaatatacaaggaatcagacc 871
Db 677 TCTATATTTGTGTAATGATCATCAGAAACAGCT-----ATCAGATCC 723
Oy 872 agtatattacttttgaattcaaatatagtaaccttgcgcgacagtcagtgtgaaa 931
Db 724 AGTATTTCACCTTTGAGCTTCAAAATATATGTTAAACCTTGGCCGACATC----- 775
Oy 932 tatctacttactcggagagatcatgtaaatatagctgaatgagacatcctttg 991
Db 775 TATCTTACTTTTACTCGGAGAGCTTCATGTAATTTAAGCTGAATGACATACCTTTG 834
Oy 992 tttagcggtgacctatccagcaggtgtttgattataaattgatacagaagaat 1051
Db 835 -----GGACCTATTCCAGCAAGCTGTTTATGTAATGATGATGATGATGATGATGAT 885
Oy 1053 gatctaccgaagaacagggagatttggtagctgtacagttgaaatagaacataca 1111
Db 866 GATCTCTCC-----TTGGAGCTGTGATCAAGTTGAATGAATGAATGAATGAATGA 928
Oy 1112 ccttgaacaacacgaagaacccgaatataagatttttagtgaattatgctttgta 1171
Db 929 CTTTAAACACAAATGAACCCGA-----CAATTATGCTTTGTA 969
Oy 1172 gtaaggaagaatgaaatattatgtctcagatgacgaatttggcagaagaatcaagta 1231
Db 970 GTAAGAGCAAGAGATATTTATTGCTCAGATGACGGAATTTGG-----A 1015
Oy 1232 gtaagtgagtgataaacaatgctggaaggtggaagcctatcagaagaacttgcta 1290
Db 1016 GTGAGTGAAGATGAACATGCTGGAAGGTGAAGACTATGCAAAACCTTGCTA 1074

REFSEQ: 11
V22702
AC V22702 standard; DNA; 947 BP.
DE Construct containing mature Interleukin-13 binding protein gene.
KW Therapeutic; IL-13 mediated condition; allergy; asthma; diagnosis;
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..947
FT FT /*tag= a
FT FT /product= "Mature IL-13 binding protein"
FT FT /note= "No stop codon given"
PN M09810638-A1.
PR 19-MAR-1998.
PR 10-SEP-1997; AU0591.

```


27-FEB-1997; AU-005374.
 10-SEP-1996; AU-002262.
 (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
 DR WPI: 98-207062/18.
 DR P-SDS: W56261.
 PT New isolated interleukin-13 binding protein - used to develop
 PT products for therapy e.g. for allergic conditions such as asthma or
 PT for diagnosis or detection
 PS Disclosure: Page 19-20; 69pp; English.
 CC The IL-13 binding protein and related therapeutic molecules can be used
 CC in the antagonism of at least one IL-13 activity. They can be used for
 CC treating IL-13 mediated conditions such as certain allergic conditions
 CC such as asthma or to inactivate locally administered IL-13 after IL-13
 CC treatment. The products can also be used as diagnostic agents, e.g. for
 CC detecting autoimmune diseases. The antibodies can also be used for
 CC immunotherapy and may also be used as a diagnostic tool.
 SO Sequence 947 BP; 312 A; 161 C; 198 G; 276 T;

Query Match 38.7%; Score 595; DB 1; Length 947;
 Best Local Similarity 82.7%; Pred. No. 8.7e-153;
 Matches 942; Conservative 0; Mismatches 0; Indels 197; Gaps 15;

QY 152 gagataaagttaacccctcccaagatttgaagatgattgaagaagaccgcat 211
 |||||
 DB 1 GAGATAAAGTTAAACCTCCACAGATTGAGATAGTGAT-----CCCGGAT 49
 QY 212 actaagttatctctatttgaatgcaaccacacgctctcgtgcatcttgtgtc 271
 |||||
 DB 50 ACTAGGTATCTCTATTTCGAATGCACCCACCTGCTCTGATCATTTT----- 103
 QY 272 gaaaggaatgcacagtggaatbatgaataaatacgaacattgtgtagaacaatgca 331
 |||||
 DB 103 --AAGGATGACAGTGAATATGACTAAATACCGAAACATGTGATGGAACATGGA 160
 QY 332 agagtagtgtaggttacatcatcttctagaatctacattaaagaatgggtttgac 391
 |||||
 DB 161 AG-----ACCATCTATTCTAGAAATTCATTCACAAAGATGGGTTTATC 205
 QY 392 ttaacaaaggcatgaaattatagaaggcgaaatatacacacgctttaccatggcaatgc 451
 |||||
 DB 206 TTAACAAGGCGCATGAA-----GCGAAGATACACAGCGCTTTACCATGGCAATGC 255
 QY 452 acaaatggaatcagaagatcagaatccaatttccatgtcagagtgggcgaaactactattgg 511
 |||||
 DB 256 ACAAAATGATCAGAAAGTTCAAAAGTTCC-----TGGCGAGAAACTACTTATTGG 303
 QY 512 atatacacaagaatccagaactaagaattcagattgaatttgggtagaatggat 571
 |||||
 DB 304 ATATCACCAAGAAATTCAGAAACTAAAGTTCAAGAT-----ATGAT 348
 QY 572 tgcgtatatacaatggcaatttctactgttcttggaaactggtcataggttaccatt 631
 |||||
 DB 349 TGGGTATATTACATTTGGCAATATTACTGTTCTTGGAAACCTGGCAATAGT----- 403
 QY 632 atgtcgtggaactcttgataccaataaactgttttactggtatggaggttgatc 691
 |||||
 DB 403 -----GTACTCTTGATACCAATTTACACTGTTTACTGTTGAGGGGTTTGATC 454
 QY 692 atgcataataatatttggaaacagtggttgatcacaaagcggtgaggaataat 751
 |||||
 DB 455 ATGCATTT-----ACAGTGTGTGATTACATCAAGCGTGAATGACAAATAT 500
 QY 752 aggatgcagaattccctatttggcgaataaaggcagtgagatcagaactaaagatt 811
 |||||
 DB 501 AGAGTGCAGATTTCCCTATTG-----GAGGCATCAGACTTAAGAT 544
 QY 812 tctataatgtgttaatgatactcagagaagaagctgaatatcaagaatcagatcc 871
 |||||
 DB 545 TCTATATTGTTGTTAATGATCTCAGAGAACAGCT-----ATCGATCC 591
 QY 872 agtatttcaactttcagctcaaaatagtaaaccttgcgcagtcagttgga 931

DB 592 AGTATTACCTTTTCAGCTTCAAAATATAGTTAAACCTTGGCCGACGTC----- 643
 QY 932 tatctacttctactcggagagtgatcagtaaatgaatgaagagacatcttg 991
 |||||
 DB 643 TATCTACTTTTACTCGGGAGAGTTATGTAATTAAGTGAATGAGACATACCTTTG 702
 QY 992 tttaggggtgacctatccagaagtggtttgattatgaatgaatgagacagaat 1051
 |||||
 DB 703 -----GGACCTATTCAGCAGAGGTGTTGATTATGAATTAAGATGAGAGAT 753
 QY 1052 gatatacacaagaatcagagatttggtagctctcagattgaatgaataacatata 1111
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 DB 754 GATACCTACC-----TTGGTACTCTCTACAGTTGAAATGAAATACATACA 796
 QY 1112 ccttgaacaacaatgaacccgaataatagatttttagtaagaatgatcttga 1171
 |||||
 DB 797 CCTGAAACACAAATGAACCCGA-----CAATATGCTTTGTA 837
 QY 1172 gtaagaacgaatgaaatttatttgcctagatgaacgaatttggcaagaataca 1231
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 DB 838 GTAAGAAGCAAACTGAATATTATGCTCAGATGACGGAATTTG-----A 883
 QY 1232 gtgagtgagtgataacaatgctgggaagtggaagactcagaagaacttgcta 1290
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 DB 884 GTGAGTGGATGATTAACAATGCTGGGAAGTGAGACCTATCGAAGAAACTTTGCTA 942

RESULT 12
 V89756
 ID 789756 standard; cDNA; 456 BP.
 AC V89756;
 DV 15-FEB-1999 (first entry)
 DE EST clone CS520.
 KW Human, secreted protein; expressed sequence tag; EST; hematopoiesis;
 KW tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
 KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
 KW gene therapy; ss.
 OS Homo sapiens.
 PN W09845436-A2.
 PD 15-OCT-1998.
 PF 10-APR-1998; U06955.
 PR 10-APR-1997; U5-838821.
 FA (GENM) GENETICS INST INC.
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D,
 PI Racie JA, Spaulding V, Treacy M;
 DR WPI: 99-070077/06.
 PT New polynucleotides encoding human secreted proteins - derived from
 PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
 PT ovary, pituitary, retina and colon cDNA libraries.
 PS Claim 1; Page 320; 618pp; English.
 CC The present sequence represents a human expressed sequence tag (EST).
 CC The polynucleotide, which is a secreted EST, and the encoded protein
 CC are predicted to have useful biological activities which would make
 CC them suitable for treating, preventing or ameliorating medical
 CC conditions in humans and animals, although no supporting data is
 CC given. Suggested activities include nutritional activity, immune
 CC stimulating or suppressing activity, hematopoiesis regulating
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
 CC activity, receptor/ligand activity, anti-inflammatory activity,
 CC cadherin/tumour invasion suppressor activity, tumour inhibition
 CC activity. The polynucleotide may also be useful for gene therapy.
 SO Sequence 456 BP; 142 A; 93 C; 92 G; 129 T.

Query Match 18.6%; Score 287; DB 1; Length 456;
 Best Local Similarity 85.6%; Pred. No. 4.8e-69;
 Matches 429; Conservative 0; Mismatches 0; Indels 72; Gaps 7;

QY 22 aggaatatacgaatttaactcggagaatggtcattatgttgcgtgcatcgg 81
 |||||
 DB 21 AGGCAATATCAAGTTTAAATCTCGAAGAAATGCT---TTGCTTGTGCTGATCGG 77

SQ Sequence 473 BP; 134 A; 92 C; 114 G; 131 T;

Query Match 14.48; Score 221.6; DB 1; Length 473;

Best Local Similarity 80.58; Pred. No. 3.1e-51; Matches 352; Conservative 0; Mismatches 35; Indels 50; Gaps 6;

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OY 2 gtgcctgcggcgaggagaggaaggaatcaatcaaggcttcaatcgcgagaatgcttaa 61
   |||||||
Db 76 gtgcctgcggcgaggagaggaaggaatcaatcaaggcttcaatcgcgagaatgcttaa 133
   |||||||
OY 62 ttgcttgcctgcgagcgtatgcttatataccttctgataagcacacacattggctgt 121
   |||||||
Db 133 ttgcttgcctgcgagcgtatgcttatataccttctgataagcacacacattggctgt 192
   |||||||
OY 122 acaagctttgcaatcattcctcagacagagataaaagttaacccctcccaagatttt 181
   |||||||
Db 193 -----ACTTCATCTTCAGACACCGAGATMAAGTTAACCTCTCAGGATTTT 240
   |||||||
OY 182 gagatagtgatlatgaaagagaaacccgataactaggtatctctatttggatggcaac 241
   |||||||
Db 241 gagatagtgatlatgaaagagaaacccgataactaggtatctctatttggatggcaac 289
   |||||||
OY 242 cccacactgctctggaatcatttggcttggaaagaaatgacagtggaatatagaactaa 301
   |||||||
Db 290 cccacactgctctggaatcatttggcttggaaagaaatgacagtggaatatagaactaa 340
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OY 302 aatacgaataatggtagtgaaacaaaggaagagctagtgtagaaggttaaccatctacta 361
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Db 341 AATACCGAATGATGAGTGAATGGAAG-----GACCATCATTA 387
   |||||||
OY 362 agaattcacattacaagatgggttggatcttaacaaggagcatggaatataagaagcg 421
   |||||||
Db 388 AGAATCTACAT--TACAAAGGATGGGCTTGGATCMTTAACAAGGGCATTGAAGCGGA 445
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OY 422 aagatacacacgctttt 438
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Db 446 AGTTACACACGGT 462

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Job time: 4119 sec

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RESULT	1			
AI798934/c				
LOCUS				
DEFINITION				
AI798934	676 bp	mRNA	EST	06-JUL-1999
W694E04.x1	Soares.NF-T.GBC.S1	Homo sapiens	CDNA	clone
IMAGE:234876.3	similar to SW:112	HUMAN O1467	INTERLEUKIN-13	
RECEPTOR ALPHA-2	CHAIN	PRECURSOR	;	mRNA sequence.
AI798934				
ACCESSION				

KEYWORDS EST. 81:5364406
SOURCE human.

ORGANISM	REFERENCE
<i>Homo sapiens</i>	1 (bases 1 to 676)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia	
Eutheria; Primates; Catarrhini; Hominoidea; Homo.	

TITLEgoi,ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
JOURNAL	Tumor Gene Index
COMMENT	Unpublished (1997). On Jun 5, 1998 this sequence version replaced

replaced gt:3169012.

Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 This clone is available royalty-free through LNL; contact the
 IMaE Consortium (info@mae.llnl.gov) for further information.
 Seq primer: -40Up from Gibco
 High quality sequence stop: 468.
 Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_id="Soares_NFL_T-GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: p1773D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP GCBI) were mixed and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. Clones 297480-302087, 602632-607239,

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BASE COUNT	ORIGIN
726408-728711, and 729096-731359. Subtraction by Bentic Scares and M. Fatima Bonaldo. "	205 a. 133 c 117 g 221 t

Query Match 27.7%; Score 426.2; DB 60; Length 676;
Best Local Similarity 82.6%; Pred. No. 3.5e-92;
Matches 660; Conservative # 0; Mismatches 13; Indels 126; Gaps 10

QY 741 ggacaaatatagtgtcagattccctatttggcataaagagcagtggagctcaga 800
|||||
Db 676 GGACAAATATAGGTGATGCAGATTTCCTATTG-----AGGCTTGA 633

QY 801 catataagattcttcattatgttgyltaatggatcatcatacagaacaaacctgaataatcaag 866
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 632 CTAATGAGATATCTATTGTGTGAATGGATCATCAGAACGAGCCT----- 583

Db 583 -- ATCAGATCCAGTATTTCCTGCTGACCTTCAAAATATAGTTAAACCTTGGCCGCAG 526

DB 525 TC -----TACTTACTTTACTCGGAGAGTTTCATGTGAATAAAGCTGAAATGCA 475

1041 tcagagagatgatactaccggaacatggaggaatttggtagctctacagttgaaa 1100
|||||
423 TCACAGAGATGATACCAC-----TTGGTACTCTACAGTTGAAA 381
|||||

[illegible]

1221	agaatcaagttagtgagtgatgataacaacatgctgggaaggtgaacacctatcgaaga	1280
339	TATGCTTTGATGTAAGAAGCAAGTGAATATTATTGCTCAGATGCGGAATTTGG----	283

263 -----AAGTGGTGGAGTGAATAAACAATGCTGGGAAGTGAAAAACCTATCGAAGA 234

1281 aaattgctagtagtggatcgcttctggctacacattggttcaacttaattagtc 1340

232 |||||

1341 atatttgaaccggtctgcttagtgaatgttgcgtgaagccaacacctaccocaaaatga 1400
|||||
184 aattttgaaccgctctgctt-----ttgggtgaagccaacccctaaccaaaaatga 133
|||||

1401 ttcccgaaattttctgtgatacatgaagaatttgcactttccatacgaagacatg 1460
|||||
132 ttccgaattttttctgtatcatgaga-----ctttccattatcaagacatg 83
|||||

1521 atttttttgcgaatgttg 1539
 82 GTATTGACTCAACAGTTCCAGTCAGTGCACCAATATGTCATATATGATGCTCAATTAACCTGA 23

22 AITTTTAAAGCAATGTC 4

Accession	Length	Organism	Source
AF358911	479 bp	Human	15-FEB-1999
U91960.05.x1	NCI CGAP_Brn23	Homo sapiens	IMAGE:2012456
	similar to SW-1122	HUMAN 014627	INTERLEUKIN-13 RECEPTOR ALPHA-2
	CHAIN PEPTIDE	ORF	mRNA sequence

ACCESSION	A1358911
NID	94110532
VERSION	A1358911.1
KEYWORDS	GT:4110532
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
TITLE	Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL	1 (bases 1 to 479)
COMMENT	NCI/NINDS-CCAP http://www.ncbi.nlm.nih.gov/ncicgap .
	National Cancer Institute / National Institute of Neurological
	Disorders and Stroke, Brain Tumor Genome Anatomy Project
	(CCAP/BTCAP), Tumor Gene Index
	Unpublished (1998)
	On Aug 21, 1998 this sequence version replaced.

Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/DBP/Image/Image.html

Insert Length: 1039 Std Error: 0.00
Seq primer: -40UP from G1bco
High quality sequence stop: 324.

FEATURES	Location/Qualifiers
source	1. .479

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="2012456"
/clone_l1b="NCI_CGAP_Brn23"
/tissue_type="gliblastoma (pooled)"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGCAGCGCCGCGCAATCTTTTTCCTTTTTCCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

```

Query Match	19.7%	Score 303;	DB 45;	Length 479;
Best Local Similarity	82.4%	Pred. No. 1.2e-62;		
Matches 468;	Conservative	0;	Mismatches 11;	Indels 89;
				Gaps 7.

Qy	965	atlaagctggaatgagacaacacttggtttaggcgcygagccattccaaagaggtctt	1025
Db	479	ATTAACTGAAATGAGACACTTT-----TGGCCCTATCCAGCAAGGTGTTT	430
Qy	1025	gattatgaatltgagatcagaagaatgtatcactccgaagaagcatygaaggaatttggta	1084
Db	429	GATTATGANNTTGATGCAGAGAAGATGATCTACC-----TTGGTGA	387
Qy	1085	ctgtctaacgtttgaaatgaaacatacacttggaaaaacaacaatgaaaccggaataatag	1144
Db	386	CTGCTACAGTTGAAAATGGAAACATACGCCCTTGAAAAACAACAAATGAAACCGA-----	333
Qy	1145	agttttagtagagatatctcttggtagaagaagaagtgatattattgtccagat	1204
Db	333	-----CAATTATCTTTGTGATGAGACGAAGCAAGTGAATTTATTTGCTCAGAT	286

Qy	1205	gaacgaattcggggcaagaagatcaagcagcagcagcggagcggagcggatataacaacatcctcgggaagcgtg	1264
Dp	285	GACGGAATTGCG-----AGGAGAGGAGAGTATATAAACATACCTCGAAGGTG	240
Qy	1265	aagaccatcggaaagaacacttcgtcagtagctggaatcgcttcctgcgtaccatcttgattt	1324
Dp	239	AAGACGTATGCGAAGAAACCTTGCTA-----CGTTTCTGGCTACCATTTGGATT	191
Qy	1335	catctataatattagttatatttctgtaacccggtctgctttagtgaaatgctgcgtaaagccaac	1384
Dp	190	CATCTTATATTAGTTATTATTGTTAAACCGGTCTGCTT-----TTGCGTAAAGCCAAC	139
Qy	1385	accacacaaaataggatccagaatctttctcgtgatacagaagaagattgcaccttc	1444
Dp	138	ACCTPPCCCAAAAAGATTCAGAAATTTTCTTGATACATGAGA-----CTTTC	89
Qy	1445	catacaagaagacatggtattgactcaacagttccacgttcacgtcgcatacggccaatggtcaatg	1504
Dp	88	CATATCAAGACACTGGTATTGACTACCTACACAGTTTCCAGTCATAGCCCAATGTTCAATATG	29
Qy	1505	agctcataaactcgaattttttcttcgcg	1532
Dp	28	AGTCGCAATAAATGATTTTTCATGAG	1

RESULT	3				
AA090507/c					
LOCUS					
DEFINITION	AA090507	443 bp	mrna	EST	23-JUN-1998
	016611.s1	Soares,NFL.T	GBC.s1	Homo sapiens	CDNA clone
	IMAGE152367.3	'	similar to SW1132_HUMAN	014657	INTERLEUKIN-13
	RECEPTOR ALPHA-2	CHAIN	PRECURSOR ;,	mrna	sequence.
REMARKS					

ACCESSION	AA909507
NID	93048912
VERSION	AA909507.1
	GI:3048912

KEYWORDS
SOURCE
ORGANISM

REFERENCE

ARTICLES
NOTED
JOURNAL
COMMENT

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2152842.

Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nh.gov
 This clone is available royalty-free through LINL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert length: 609 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 220.
 Location/Qualifiers
 1..443

/db_xref="taxon:9606"
 /clone="IMAGE:1523637"
 /clone_id="Soares_NFL_T_GBC_S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBHL9W, testis NH7, and B-cell
 NCI-GCAP GCBI) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 682632-687339,
 726608-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonafide. "

BASE COUNT	134 a	88 c	74 g	147 t
ORIGIN				

Query Match	19.5%	Score 300;	DB 40;	Length 443;
Best Local Similarity	84.7%;	Pred. No. 6e-62;		
Matches 439;	Conservative 0;	Mismatches 0;	Indels 79;	Gaps 6

This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.jlni.gov) for further information.
 Insert Length: 665 Std Error: 0.00
 Seq primer:-40m13 fwd. ET from Amersham
 High quality sequence stop: 242.
 Location/Qualifiers
 1 360

Source

1. 200
2. 200
3. 200
4. 200
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99. 200
100. 200

Homosapiens

/db_xref="taxon:9606"

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map="8"
```

```
/clone="IMAGE:1030867"
```

```
/clone lib="Soares testi
```

```
sex="male"
```

```

/proc mount= "DH10B"

```

/1au_103c - D11Vb

/hold - Vector: p1/I3D-Pr

polylinker; Site_1: Not

0y	1129	gaacccgcgaataatagatttttagtgcattatctcttgtgtgaagaagaatgaa	1188
Db	340	GAACCCGA-----CAATATCTCTTGTGTGTAAGACCAAAAGTGA	300
0y	1189	tattatttgctcagatgaacgaatttggsgaagaatcaagtgtgtgtgtgtatgaa	1248
Db	229	TATTATTGCTCAATATCGAATTTG-----AGTAGTGTGAGTGTATGA	254
0y	1249	caatgctcgggaagtgtagacatacgaaabaacttctagtagctcgtgttc	1308
Db	253	CAATGCTCGGAAGTGAAGACTATCGAAGAAAACTTTGCTA-----CGTTTCT	205

BASE COUNT	110 a	68 c	61 g	121 t
ORIGIN				

Query Match	16.38;	Score 250.4;	DB 36;	Length 360;
Best Local Similarity	88.48;	Pred. No. 4.6e-50;		
Matches 334;	Conservative 0;	Mismatches 1;	Indels 43;	Gaps 4

[illegible]

RESULT	4			
AA621766/c				
LOCUS	AA621766	360 bp	EST	02-MAR-1998
DEFINITION	af06d40..s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030867			
	3', mRNA sequence.			
ACCESSION	AA621766			
NID	92524194			
VERSION	AA621766.1	GI:2524194		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			

REFERENCE
1 (pages 1 to 360)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marr, M.,
Martin, J., Moore, B., Schellenberg, K., Stepien, M., Tan, F.,
Teiseling, B., White, Y., Wylie, T., Waterson, R. and Wilson, R.
Washu-NCI human EST project
TITLE
JOURNAL
COMMENT
On Sep 12, 1996 this sequence version replaced gi:1394197.

LOCUS	RS2796	465 bp	EST	18-MAY-1995
DEFINITION	Y99910.s1 Soares Infant Brain IN1B Homo sapiens cDNA clone IMAGE:416483, mRNA sequence.			

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 465)
Hiller, L., Lennon, G., Becker, M., Bernaldo, M.F., Chipelli, B.,
Chissos, S., Dierrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevisan, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478

TITLE

JOURNAL
MEDLINE
COMMENT

Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wustl.edu

Insert Size: 1454

High quality sequence stops: 382 Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1454 Std Error: 0.00

Seq primer: Promega -21m3

High quality sequence stop: 382.

FEATURES

source

1. 465

/organism="Homo sapiens"

/db_xref="GDB:414189"

/db_xref="taxon:9606"

/clone="IMAGE:41648"

/clone_lib="Soares Infant brain INIB"

/sex="Female"

/dev_stage="73 days post natal"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: whole brain; Vector: Lambda BA; Site: 1: Not

I; Site: 2: Hind III; 1st strand cDNA was primed with a Not

I - oligo(dT) primer [5';

ACTGCAAGATTCGCGCGCGCGGAGATTTTCTTTTCTTTT 3'];

double-stranded cDNA was ligated to Hind III adaptors

(Pharmacia), digested with Not I and directionally cloned

into the Not I and Hind III sites of the Lambda BA vector.

Library went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bernaldo."

BASE COUNT

135 a 92 c 79 g 158 t 1 others

ORIGIN

Query Match

15.8% Score 242.4; DB 22; Length 465;

Best Local Similarity 83.9% Pred. NO. 3.8e-48; Indels 62; Gaps 7;

Matches 381; Conservative 0; Mismatches 11;

1088 ctcaagctgtaaaatgaaacataca-ccttgaagaacaaatgaaccggaataatag 1146

405 CTACAGTTGAAATGAAACATACACCTTGAAACAAATGAAACCGCATTTATGC 346

1147 ttttagtaagcaatcattgcttctgtagtaagaagaatgtaattctatctc-cagaatg 1205

345 -----CTTTGTAGTAAGCAACCAAGTGAATTTATTTCTCCACATG 304

1206 agcgaattggcgaagaatcaatagtagtagtagtagtagtaacaatgctggaagtaga 1265

303 AGGGAATTTGG-----AGTGAAGTGAAGTGAATTAACAAAGCTGGAAGGTGA 258

1266 agacctatcagaagaactgctagtagcgggagctcttctgctacccattggttgc 1325

257 AGACCTATCGAAGAAACATTTC-----CTACGTTTCTGGCTACCATTTGCTTTC 208

1326 attctaattatgattatattgtaaccggtctgcttagtagtaatttgcgtaagcaaca 1385

207 ATCTTAATATATAGTATATTGTGAACCGGTCTGCTT-----TTGCGTAAGCAACAA 156

QY 1386 cctcgcgaagaatcattccagaattttctctgatatacatgaagaattgcatcttcc 1445

DB 155 CTTACCCAAAATGATTCGCAATTTTCTGTGATACATGAAGA-----CTTCC 106

QY 1446 atcacaagacatgattgattgacccaacagttccagttcattggtcgaatttcaatga 1505

DB 105 ATATCAAGACAGCATGATGATGACATCAACATTTCCATCATGCGCAATGTCAAAATTA 46

QY 1506 gtcccaataactgaattttcttctgcaatgttg 1539

DB 45 GTCTCAATTAACGTAATTTTCTTGGCAATGTG 12

RESULT 6

AW001800/C 446 bp mRNA EST 08-SEP-1999

DEFINITION w505601.x1 NCI-CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2496288 3'

similar to SW:1132.HUMAN Q14627 INTERLEUKIN-13 RECEPTOR ALPHA-2

CHAIN PRECURSOR ; mRNA sequence.

ACCESSION AM001800

NID 95848716

VERSION AM001800.1 GI:5848716

KEYWORDS EST.

SOURCE human

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 446)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On May 18, 1998 this sequence version replaced gi:3136930.

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmett-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/dbp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 384.

Location/Qualifiers

1. 446

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2496288"

/clone_lib="NCI-CGAP_Kid1"

/lab_host="DH10B"

/note="Organ: kidney; Vector: pV73P-Pac (Pharmacia) with

a modified polylinker; Site: 1: Not I; Site: 2: Eco RI;

Plasmid DNA from the normalized library NCI-CGAP_Kid1 was

prepared, and ss circles were made in vitro. Following HAP

purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs

from a pool of 5,000 clones made from the same library

(cloneids 1322376-1323911, 1456007-1456775, and

1500552-1502855). Subtraction by Bento Soares and M.

Fatima Bernaldo.

BASE COUNT 136 a 85 c 75 g 145 t 5 others

ORIGIN

Query Match

15.5% Score 239; DB 63; Length 446;

Best Local Similarity 88.1% Pred. NO. 2.5e-47;

Matches 333; Conservative 0; Mismatches 1; Indels 44; Gaps 5;

QY 1157 caattatgcttctgtaagaagaagcaagatgatatattatgctcaagatggaatttg 1216
 Db 335 CAATTAATGCTTTAGTAAGAAACCAAGTAAATTAATTTATGTCAGATACGAAATTTGG 276
 QY 1217 gcaaaagaatcaagtagtgaagtgatgaataaacaatgctgggaagggtgaagactatga 1276
 Db 275 -----AGTGTGAGTGAAGTAAACCAATGCGGAGGTGAAGACCTATGCA 230
 QY 1277 agaaaacttctgtagtgcggagctgttctgctgacacatttggtttcaattatatt 1336
 Db 229 AGAAACTTTCCTA-----CGTTCTGGCTACCACTTTGTTTCTATCTTAATTT 181
 QY 1337 agtataattctgaacccgctccttgatgaatgttgctgaagccaacacccacaaa 1396
 Db 180 AGTTAATTTGTAACCGGTCTGCTT-----TTGGCTAACCACCAACCTACCCAAA 129
 QY 1397 atgattccagaattttctgtagatataagaagaattgcatcttccatacaagaaga 1456
 Db 128 ATGATTCAGAAATTTTCTGTGATACATGAGA-----CTTCCATATCAAGAGA 79
 QY 1457 catgtatgtactcaacagtttccagtcagtcagccaatgttcaatgaagctcaa-aa 1515
 Db 78 CATGTGATGTGACTCAACAGTTCTCCAGTCATGCCCAATGTTCAATGATGCTCAACTAA 19
 QY 1516 actgaattttctgctga 1533
 Db 18 NOTGAAATTTTCTTTCGA 1

RESULT 7
 R52795 473 bp mRNA EST 18-MAY-1995
 LOCUS Y099f10.r1 Soares infant brain INIB Homo sapiens cDNA clone
 DEFINITION IMAGE:41448 5', mRNA sequence.
 R52795
 R52795.1 GI:814697
 NID 9814697
 VERSION R52795.1 GI:814697
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 473)
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chapell, B.,
 Chissoe, S., Dietrich, N., Dubucque, T., Favello, A., Gish, W.,
 Hawkins, M., Hultman, M., Kucaba, T., Lacey, M., Le, N.,
 Marais, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
 Rohlfing, T., Schellendberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
 Trevisan, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,
 and Marra, M.
 TITLE Generation and analysis of 280,000 human expressed sequence tags
 JOURNAL Genome Res. 6 (9), 807-828 (1996)
 MEDLINE 97044478
 COMMENT

CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Insert Size: 1454
 High quality sequence stops: 372 Source: IMAGE Consortium, LNL.
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert length: 1454 Std Error: 0.00
 Seq primer: M13p1
 High quality sequence stop: 372.
 Location/Qualifiers
 1. 473
 /organism="Homo sapiens"
 /db_xref="GDB:414189"
 /db_xref="taxon:9606"

/clone="IMAGE:41648"
 /clone.lib="Soares infant brain INIB"
 /sex="female"
 /dev_stage="73 days post natal"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: whole brain; Vector: latmid BA; Site: 1: Not
 1: Site: 2: Hind III; 1st strand cDNA was primed with a Not
 I - oligo(dT) primer [5',
 AACTGGAAGATTCGGCGCCGCGAGCAATTTTCTTTTCTTTT 3'];
 double-stranded cDNA was ligated to Hind III adaptors
 (pharmacia), digested with Not I and directionally cloned
 into the Not I and Hind III sites of the latmid BA vector.
 Library went through one round of normalization. Library
 constructed by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 134 a 92 c 114 g 131 t 2 others
 ORIGIN

Query Match 14.4%; Score 221.6; DB 22; Length 473;
 Best Local Similarity: 80.5%; Pred. No. 3.7e-43;
 Matches 352; Conservative 0; Mismatches 35; Indels 50; Gaps 6;

QY 2 gtgcctgctgcggaggagagagatcaatcatcaaggttttaattctggagaatggtctaa 61
 Db 76 GTGCTGTGCGGGGGGAGAGAGCAATATCAAGTITTAATCTCGGAGAAATGCT--- 133
 QY 62 ttctgttctgtgctatcgatgctgtatataaccttctgataagacacacattgctgt 121
 Db 133 TTCTGTGCTTGGCTATCGATGCTTATTAACCTTCTGATAGACAACTTGGCTGT 192
 QY 122 acaagctttgactctcttcagacacagagataaaagttaacctctcaggattt 181
 Db 193 -----ACCTCATCTTCAACACCGAGATAAAAGTTAACCTCCACAGATT 240
 QY 182 gagatagtgattatgaagaagaacccgatacttactgttactctatttgcagagaaac 241
 Db 241 GAGATAGTGAT-----CCCGATACTAGGTATCTCTATTTTCATATGCGAAC 289
 QY 242 cccacgtctctgatatatttctgtgtgtaagaagaatgcagatgaaatgaactaa 301
 Db 290 CCCACGTCTCTGTGATCATTT-----AAGGATGCACAGCTGATATGAACTAA 340
 QY 302 aatacgaacattgtgtagtgaacaacatggaagcttagtgaaggtttacacataacta 361
 Db 341 AATACCGAAACATTGGTAGGAAACATGGGAG-----GACCATATTACTA 387
 QY 362 agatctacattcaaaagaatggtttgattcttaacaaaggcatgaattatagaagggc 421
 Db 388 AGAATCTACATT--TACAAAGATGGGCTTGGATCATTAAACAGGGCATGAAGCGCA 445
 QY 422 aagatcacacagcttt 438
 Db 446 AGTTACACACAGGTTT 462

RESULT 8
 AA298563 365 bp mRNA EST 18-APR-1997
 LOCUS EST114178 HSCI172 cells I Homo sapiens cDNA 5' end similar to IL13
 DEFINITION receptor (IL13R), mRNA sequence.
 R52795
 R52795.1 GI:1950896
 NID 91950896
 VERSION AA298563.1 GI:1950896
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 365)
 AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
 Bull, C.J., Lee, N.H., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man, Wai, C.,
 Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodet, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudak, D.M., Shiley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A., He, M.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meltsner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)

6026280
On Sep 12, 1996 this sequence version replaced g1:1393411.
Other ESTs: TRC194124
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES

Source

1. 365
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/cell_type="fibroblast"
/cell_line="HSC172 (16PDL)"
/dev_stage="fetal"
/note="Organ: lung; Vector: pBluescript SK-; Site: 1;
EcoRI: Site 2: XhoI"

BASE COUNT 106 a 66 c 69 g 123 t 1 others

ORIGIN

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Best Local Similarity 82.0%; Pred. No. 5.3e-40;
Matches 342; Conservative 0; Mismatches 2; Indels 73; Gaps 6;

507 attgataaccacacgaagattccgaactaaagttcagatttaagtttggtagaa 566
1 ATTCGATATACACAGAGATTCCAGAACTAAGTTCAGAGAT-----A 45

567 tggattcgatatatacaattggaataattactctgttcttggaaacctggcagatt 626
46 TGGATTGCGATATATACAAATGCAATATTACTCTGTTCTGGAAACCTGGCATAGGT- 105

627 acattatgctgggtactctctgtatcaaatatacaactgtttactggtatagggtt 686
105 -----GTACTCTCTGATACCAATTACACTGTGTTTACTGATAGAGGCTT 151

687 ggaatcatgataataatatttggaacacgtgtgtattacatcaaggcgtgtagaaca 746
152 GGTTCATGACAT-----ACAGTGTGTGATTACATCAAGCGTGAAGGACAA 197

747 aatagagatgcaattccctatttggcaataaaggagcgtgtagcactatgaat 806
198 AATATAGAGATGACATTCCTATTG-----GAGGATCAGACTATTA 241

807 agattcctatatgtcttaatgatatcatgagagaacagcgaatatacaagaatca 866
242 AGATTCTATTATTGTTGTTAATGATCATCATGAGANCAAGCCT-----ATCA 288

QW 887 gatcccttattactt-ccgttcaaatatagtttaaaccttgcgcagtc 922
DB 289 GATCCCTATTATTACTTTCACCTTCACCAAAATATACTTAACCTTCCGCCAGTC 345

RESULT

9

ACCESSION AF701600 469 bp DNA GSS 27-JUL-1999
VERSION AF701600.1 GI:5627410
KEYWORDS GSS
SOURCE Human
ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 469)
Mendiras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Furlong, J., Shaker, R., Schmidt, S., Traicoff, R., and Hood, L.E.

TITLE

Construction of a Characterized Clone Resource for Genomic Sequencing
Unpublished (1998)

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

FEATURES

1. 469
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Plate-3132 Col=9 Row=D"
/clone_lib="CIR Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10F"

BASE COUNT

149 a 78 c 84 g 150 t 8 others

ORIGIN

Query Match 4.9% Score 75; DB 89; Length 469;
Best Local Similarity 82.4%; Pred. No. 5e-08;
Matches 117; Conservative 0; Mismatches 6; Indels 19; Gaps 2;

1260 aggtgaagacctatcgagaagaactgtcagtagcggagatgcttgcgtacactt 1319
272 AGGTGAAGACCTATCGAAGAGACTTGTCTA-----CGTNTGCTACCATTT 320

1320 ggtttccttaatatagttatattgttaacggctgtgtatgtaattgctgtaagc 1379
321 GGTTCATCAATTAATATAGTTAATAAGTAAACGGGTGCTT-----TTGGTAGC 372

1380 caaacacctaccacaaatgat 1401
373 CAACACCTACCCAAATAGT 394

RESULT 10
CNS00396/c 1101 bp DNA GSS 03-JUN-1999
LOCUS
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #

genomic survey sequenced

ORGANISM *Drosophila melanogaster*

TITLE
Direct Submission
Submittal

library (Dros BAC) was made by

source	1. .1204
--------	----------

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PAGE CONTNT : 300 - /note="end : T7"
122

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Matches 111; Conservative 150; Pred. No. 0.0054;

855 atcaaggaatcagatccagtatttcatttcaaccttcaaaattatattt

1083 KWAALAKWKATKKDDDDDKKAA⁴DAKKKKKKAKAKADADKAAADKKDKKKAKADAWDDADDDAAK 1094

RESULT 12
A1547789
LOCUS
DEFINITION
ACCESSION
MID
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

A1547789 160 bp mRNA EST 22-MAR-1999
UI-R-C3-s4-h-02-0-UI.s1 UI-R-C3 Rattus norvegicus cDNA clone
UI-R-C3-s4-h-02-0-UI 3', mRNA sequence.
A1547789
94465277
A1547789.1 GI:4465277
EST.
Norway rat.
Rattus norvegicus
Euthyrola; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 160)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (?), 791-805 (1996)
97044477
On Jun 5, 1998 this sequence version replaced gi:3187484.

CONTACT: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel.: 319 335 8250
 Fax: 319 335 9565
 Email: mosaics@blue.weeg.uiowa.edu
 Oligo-dT track not found. Not I site shown in beginning of sequence
 is likely internal to the message. cDNA library Preparation: M.B.
 Soares lab clone distribution: clones will be available through
 Research Genetics (www.resgen.com)
 Seq primer: M13 Forward,
 Location/Qualifiers
 1..160

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/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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/clone_id="UI-R-C3"
/seq_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: p7172 Pac (Pharmacia) with a modified
polylinker. Site_1: Not I. Site_2: Eco RI. The UI-R-C3
library is a subtracted library of a series, ultimately
derived from a mixture of individually tagged normalized
libraries from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day
embryos, after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: UI-R-C3, UI-R-Cp,
UI-R-Cl, UI-R-CO, UI-R-Al, UI-R-EI. The tag is a string of

```

3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C3) was constructed as follows: PCR amplified cDNA inserts from UI-R-C2p clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-C2p library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C3 library. This procedure has been previously described (Bonaldi, Lennon and Soares, Genome Research 6:791-806, 1996)."

Query Match	3.2%	Score 48.6;	DB 48;	Length 160;
Best Local Similarity	65.1%;	Pred. No. 0	1;	
Matches 114;	Conservative	0;	Mismatches	39;
			Indels	22;
			Gaps	2;

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Cy      805 aaagaattctatataattgttgtaatgatcatcagaaacaacccgtaaatatcaaggaat 864
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       8 AAAGCTTTTATTTCGTATGATGCACCAAAAGCTGAGCCT-----AT 54
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```

Gen. 865 CGAGCCAGTATTTCACCTTTCAGCTCAAAATAGTAAACCTTGCAGCCAGTCAG 924
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Eib 55 CATATCCAGCTACATGGTTTTCACCTCAAAATATAATTAACCACTTGCCACAG---- 1111

```

925 ttggaataatcttactttactcggagaggttcacgtgaaatcaatgcgaatatg 979
+
D8 .11 -----ATTCCCTATATTACTGTGAGAACTCTATTGCATTCGAATGAATGG 160

| LOCUS | DEFINITION |
|-----------|---|
| RECT1 13 | |
| CN6016FP | |
| CNS116FP | 1201 bp DNA |
| BACN15K18 | Drosophila melanogaster genome survey sequence T7 end of BAC |
| | Drosophila melanogaster (fruit fly), genomic survey sequence. |
| | 26-JUL-1999 |

| | |
|-----------|------------|
| ACCESSION | AL106687 |
| NID | 35623252 |
| VERSION | AL106687.1 |
| | GI:5623252 |

| ALIMONDS | 688. |
|----------|-------------------------|
| SOURCE | fruit fly. |
| ORGANISM | Drosophila melanogaster |

EXPERIENCE: 1 (bases 1 to 1201)

Genoscope - Centre National de Sequençage :
Submitted (23-JUL-1999)
Direct Submission
Genoscope
JOURNAL
BP 191 91006 Evry cedex - FRANCE (E-mail : secretf@genoscope.cns.fr)

COMMENT
new: www.genoscope.cns.fr
determination of this BpC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Balland at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

```

FEATURES
  source
    Location/Qualifiers
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        /plasmid="pBelosBAC11"
        /db_xref="taxon:7227"
        /clone_l1b="DrosBAC"
        /clone="BACN15K18"
        /note="end : 77"
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        171 c
        199 g
        357 t
        197 others

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Best Local Similarity 31.0%; Pred. No. 0.87;
Matches 91; Conservative 81; Mismatches 117; Indels 5; Gaps 1;

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Qy 1018 gtgttttgaattgaatgagatgatactaccgaaagcatgaggatt 1077
      ::::: | | | | | | | | | | | | | | | | | | | | | |
Db 1089 KKKKGAKAGTAAAKAKKADADADADADADADADADADADADADAD 1030
      ::::: | | | | | | | | | | | | | | | | | | | | | |
Qy 1078 ttggtgactgctacagctgaataatgaacatacaccttgaacaacaatgaacccga 1137
      ::::: | | | | | | | | | | | | | | | | | | | | | |
Db 1029 KKKAKADKAAAKAKKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 970
      ::::: | | | | | | | | | | | | | | | | | | | | | |
Qy 1138 ataataagagtttttagtagcaatttgctt-----gtagtaagaagcaagtgatatt 1192
      | | | | | | | | | | | | | | | | | | | | | |
Db 969 AAAAAAAAAAAAAAAAAAKAADAADADADADADADADADADADADAD 910
      ::::: | | | | | | | | | | | | | | | | | | | | | |
Qy 1193 tattcctcagatgacggaatttgggcaagaatcgaagtagtgagtgatgaacaat 1252
      | : : | | : | | : | | : | | : | | : | | : | | : |
Db 909 AAKAKRAAAAKAKADADADADADADADADADADADADADADADDD 850
      | : : | | : | | : | | : | | : | | : | | : | | : |
Qy 1253 gctgggaaggtgaagaccatcgaaagaaacttgctagtagtgagtgatgctt 1306
      | | | | | | | | | | | | | | | | | | | | | |
Db 849 AKAARAAAKAKKAAKAAKAAKAAKADADADADADADADADADADAKK 796
      | | | | | | | | | | | | | | | | | | | | | |

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Search completed: January 20, 2000, 05:25:26
Job time: 6339 sec

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GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 19, 2000, 20:00:50 ; Search time 34.07 Seconds
(without alignments)
296.858 Million cell updates/sec

Title: US-09-077-317-4

Perfect score: 2324

Sequence: 1 MEMPARLGLMALLLCAGGG.....QTRERTSVLIENLKASQ 427

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A_Geneseq.36.*

Word size: 0

Number of hits that pass the threshold: 188963

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|--------|----------------------|
| 1 | 2324 | 100.0 | 427 | 1 | W24973 | Human interleukin-13 |
| 2 | 2309.5 | 99.4 | 426 | 1 | W09822 | Human interleukin-13 |
| 3 | 1708.5 | 75.5 | 426 | 1 | W09821 | Mouse interleukin-13 |
| 4 | 942 | 40.5 | 177 | 1 | W58937 | Human interleukin-13 |
| 5 | 318 | 13.7 | 415 | 1 | R22211 | Sequence of Interl |
| 6 | 318 | 13.7 | 415 | 1 | R22217 | Sequence of Interl |
| 7 | 318 | 13.7 | 398 | 1 | R22212 | Sequence of Interl |
| 8 | 302 | 13.0 | 372 | 1 | W36616 | Celebicus macaque zc |
| 9 | 296.5 | 12.8 | 421 | 1 | R25064 | Human IL-5 receptor |
| 10 | 295.5 | 12.7 | 380 | 1 | W35295 | Human IL-13 binding |
| 11 | 295.5 | 12.7 | 380 | 1 | W36613 | Human zcytoz2 cyto |
| 12 | 295.5 | 12.7 | 380 | 1 | W41502 | Human cytokine/pep |
| 13 | 295.5 | 12.7 | 380 | 1 | W33603 | Human interleukin-13 |
| 14 | 295.5 | 12.7 | 380 | 1 | W24972 | Human interleukin-13 |
| 15 | 295.5 | 12.7 | 380 | 1 | W41520 | Human HR-1 recepto |
| 16 | 294.5 | 12.7 | 380 | 1 | W36614 | Human zcytoz2 cyto |
| 17 | 294.5 | 12.7 | 420 | 1 | W83842 | Human interleukin-13 |
| 18 | 293.5 | 12.6 | 420 | 1 | R22215 | Sequence of human |
| 19 | 288.5 | 12.4 | 420 | 1 | R22219 | Sequence of secret |
| 20 | 287.5 | 12.4 | 383 | 1 | W35294 | Murine IL-13 bindi |
| 21 | 284 | 12.2 | 359 | 1 | W56260 | Construct containi |
| 22 | 284 | 12.2 | 315 | 1 | W56261 | Mature interleukin |
| 23 | 282.5 | 12.2 | 396 | 1 | R22216 | Sequence of human |
| 24 | 281 | 12.1 | 396 | 1 | R22220 | Sequence of secret |
| 25 | 260 | 11.2 | 312 | 1 | R22213 | Sequence of Interl |
| 26 | 260 | 11.2 | 315 | 1 | R22214 | Sequence of Interl |
| 27 | 260 | 11.2 | 332 | 1 | R22218 | Sequence of Interl |
| 28 | 236 | 10.2 | 1026 | 1 | R70121 | IL5-R-GBP 130 fusi |
| 29 | 234 | 10.1 | 313 | 1 | W21856 | Protein used in pr |
| 30 | 229 | 9.9 | 335 | 1 | R25063 | Soluble human IL-5 |
| 31 | 229 | 9.9 | 335 | 1 | R33699 | Shit-5R-alpha. Deo |
| 32 | 228 | 9.8 | 369 | 1 | R10919 | Human GM-CSF recep |
| 33 | 205.5 | 8.8 | 369 | 1 | R59094 | Murine IL-2R gamma |
| 34 | 202 | 8.7 | 347 | 1 | R47149 | IL-2 receptor gamm |
| 35 | 202 | 8.7 | 369 | 1 | R47148 | IL-2 receptor gamm |
| 36 | 180 | 7.7 | 425 | 1 | W70962 | Rat Zcytoz5 protei |
| 37 | 178.5 | 7.7 | 482 | 1 | W31646 | Human cytokine rec |
| 38 | 178 | 7.7 | 452 | 1 | R47150 | IL-2 receptor gamm |
| 39 | 178 | 7.7 | 230 | 1 | R47151 | IL-2 receptor gamm |

| | | | | | | |
|----|-----|-----|-----|---|--------|--------------------|
| 40 | 178 | 7.7 | 230 | 1 | R82934 | Interleukin 4 comp |
| 41 | 176 | 7.6 | 630 | 1 | R93126 | Tilapia prolactin |
| 42 | 176 | 7.6 | 606 | 1 | R93121 | Tilapia prolactin |
| 43 | 175 | 7.5 | 413 | 1 | W50111 | Novel haemopoietin |
| 44 | 175 | 7.5 | 425 | 1 | W50112 | Novel haemopoietin |
| 45 | 174 | 7.5 | 425 | 1 | W59804 | Nucleotide sequenc |

ALIGNMENTS

| | | | | | |
|---|--------------|--------------------|------------|------------|--------|
| Query Match | 100.0% | Score 2324 | DB 1 | Length 427 | |
| 1st Local Similarity | 100.0% | Pred. No. 9.7e-211 | | | |
| Matches 427 | Conservative | 0 | Mismatches | 0 | Indels |
| | | | | | Gaps 0 |
| MEMPARLGLMALLLCAGGGGGGGAAPETPTPTNTLSVSTTCTVYMTNPPREGASS 60 | | | | | |
| 1 MEMPARLGLMALLLCAGGGGGGGAAPETPTPTNTLSVSTNCTVYMTNPPREGASS 60 | | | | | |
| NCSLWFSHFGRKODKRIKIPETRSIEVPLNRIICLVGSGOSTSESEPSILVKEICSP 120 | | | | | |
| 1 NCSLWFSHFGRKODKRIKIPETRSIEVPLNRIICLVGSGOSTSESEPSILVKEICSP 120 | | | | | |
| PGSDPESAVTELOCIMHNSYKSCWLPGRNTPSPNTNTLYYHRSLEKIHOCENIFREG 180 | | | | | |
| 1 PGSDPESAVTELOCIMHNSYKSCWLPGRNTPSPNTNTLYYHRSLEKIHOCENIFREG 180 | | | | | |
| QVFGGSFDLTLYKSDSSFEHSHVOIWKDAGIKISFNIVPLTSRYKPPPIKULSFHN 240 | | | | | |
| 1 QVFGGSFDLTLYKSDSSFEHSHVOIWKDAGIKISFNIVPLTSRYKPPPIKULSFHN 240 | | | | | |
| DLVYQWENPQNFISNCLFEYEVNNSQTEHNVFYQVQAKCENDEFENVENTSCFWVP 300 | | | | | |
| 1 DLVYQWENPQNFISNCLFEYEVNNSQTEHNVFYQVQAKCENDEFENVENTSCFWVP 300 | | | | | |

```

Db 241 DDLVQWENPQNFISRCLEFEVEVNSQTEHNFYVQAKCENPEFERVENTSCFMP 300
QY 301 GVLPTLTNTVIRKTKLCYEDDKLMSNMSQEMSIGKRNSTLYITMLIVPIYVAGAI 360
Db 301 GVLPTLTNTVIRKTKLCYEDDKLMSNMSQEMSIGKRNSTLYITMLIVPIYVAGAI 360
QY 361 IVLLLYLRLKLIIFPPIDPGKIFKEMFGDQNDTLHMKKYDIYEKOTKEETDSVLLIE 420
Db 361 IVLLLYLRLKLIIFPPIDPGKIFKEMFGDQNDTLHMKKYDIYEKOTKEETDSVLLIE 420
QY 421 NLKRSQ 427
Db 421 NLKRSQ 427

RESULT 2
W09822 standard: Protein: 426 AA.
ID W09822:
AC W09822:
DT 15-JUL-1997 (first entry)
DE Human interleukin-12 receptor alpha chain NR4.
KW NR4; haemopoietin receptor; interleukin-13 receptor; IL-13;
KW cytokine; allergy; asthma; therapy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..27
FT /label= Sig_peptide
FT protein 28..426
FT /label= Mat_protein
FT domain 28..118
FT /label= Extracellular domain
FT /note= "Ig-like domain"
FT modified_site 36
FT /label= N-glycosylation site
FT modified_site 104
FT /label= N-glycosylation_site
FT domain 119..342
FT /label= Haemoreceptor_receptor-domain
FT modified_site 137
FT /label= N-glycosylation site
FT region 326..330
FT /label= WSDMS_motif
FT domain 343..366
FT /label= Transmembrane_domain
FT domain 367..426
FT /label= Cytoplasmic_tail

W09715663-A1.
PD 01-MAY-1997.
PF 23-OCT-1996; A00668.
PR 23-OCT-1995; AU-006135.
PR 22-DEC-1995; AU-007276.
PR 09-SEP-1996; AU-002208.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Hilton DJ, Metcalf D, Nicola NA, Willson T, Zhang JG;
DR WPI: 97-259018/23.
DR N-PSDB: T66165.
PT DNA encoding animal haemopoietin receptor which interacts with
PT interleukin-13 - useful to treat asthma, allergy or condition
PT exacerbated by IGE production
PS Claim 5; Page 52-54; 93pp; English.
CC Novel mouse and human haemopoietin receptors (W09821 and W09822),
CC designated NR4, comprise the interleukin-13 (IL-13) receptor
CC alpha-chain. The human NR4 amino acid sequence was deduced from
CC a composite DNA sequence (T66165) derived from bone marrow cDNA
CC clones. Recombinant NR4, or fusion proteins including NR4, can
CC be produced in transformed host cells. The receptor molecules and
CC their components are useful in the development of a range of
CC agonists, antagonists, therapeutics and diagnostic reagents based
CC on ligand interaction with its receptor, esp. for the development
CC of cDps, capable of modulating the activity of IL-13 and related
CC cytokines such as interleukin-4 for the treatment of allergy, asthma
CC and other conditions relating to IGE.

```

```

SQ Sequence 426 AA:
Query Match 99.44; Score 2309.5; DB 1; Length 426;
Best Local Similarity 99.84; Pred. No. 2.3e-209;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MEMPARLGLMALLICAGGGGGGGAAPTEQPEVTMLSYVENLCVITWMPPEGASS 60
Db 1 MEMPARLGLMALLICAGGGGGGGAAPTEQPEVTMLSYVENLCVITWMPPEGASS 59
QY 61 NCSLMYFSHEDKODKKIAPETRSIEVPLNERICLOVSGQCSNSESKEKSIYKCI 120
Db 61 NCSLMYFSHEDKODKKIAPETRSIEVPLNERICLOVSGQCSNSESKEKSIYKCI 119
QY 121 PEGDPESAVTELOCIMHNLSTYKCSWLPGRNTSPDTNTLYYHRSLEKTHOCENIREG 180
Db 121 PEGDPESAVTELOCIMHNLSTYKCSWLPGRNTSPDTNTLYYHRSLEKTHOCENIREG 179
QY 180 QYFGCSFDLTKVKSSEFQSHSVQIMVKNMGKIKPSFNIVPLSRVAPDPPIKNSFHN 240
Db 180 QYFGCSFDLTKVKSSEFQSHSVQIMVKNMGKIKPSFNIVPLSRVAPDPPIKNSFHN 239
QY 241 DDLVQWENPQNFISRCLEFEVEVNSQTEHNFYVQAKCENPEFERVENTSCFMP 300
Db 241 DDLVQWENPQNFISRCLEFEVEVNSQTEHNFYVQAKCENPEFERVENTSCFMP 299
QY 301 GVLPTLTNTVIRKTKLCYEDDKLMSNMSQEMSIGKRNSTLYITMLIVPIYVAGAI 360
Db 301 GVLPTLTNTVIRKTKLCYEDDKLMSNMSQEMSIGKRNSTLYITMLIVPIYVAGAI 359
QY 361 IVLLLYLRLKLIIFPPIDPGKIFKEMFGDQNDTLHMKKYDIYEKOTKEETDSVLLIE 420
Db 361 IVLLLYLRLKLIIFPPIDPGKIFKEMFGDQNDTLHMKKYDIYEKOTKEETDSVLLIE 419
QY 421 NLKRSQ 427
Db 421 NLKRSQ 426

RESULT 3
W09821 standard: Protein: 426 AA.
ID W09821:
AC W09821:
DT 15-JUL-1997 (first entry)
DE Mouse interleukin-12 receptor alpha chain NR4.
KW NR4; haemopoietin receptor; interleukin-13 receptor; IL-13;
KW cytokine; allergy; asthma; therapy.
OS Mus sp.
FH Key Location/Qualifiers
FT peptide 1..27
FT /label= Sig_peptide
FT protein 28..426
FT /label= Mat_protein
FT domain 28..118
FT /label= Extracellular domain
FT /note= "Ig-like domain"
FT modified_site 36
FT /label= N-glycosylation site
FT modified_site 104
FT /label= N-glycosylation_site
FT domain 119..342
FT /label= Haemoreceptor_receptor-domain
FT modified_site 137
FT /label= N-glycosylation site
FT region 326..330
FT /label= WSDMS_motif
FT domain 343..366
FT /label= Transmembrane_domain
FT domain 367..426
FT /label= Cytoplasmic_tail
FT misc_difference: 21
FT /note= "unidentified amino acid"

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FT misc_difference 194
 PN /note- "unidentified amino acid"
 PD W09715663-A1.
 PR 01-MAY-1997.
 PR 23-OCT-1996; AU00668.
 PR 23-OCT-1995; AU-006135.
 PR 22-DEC-1995; AU-007276.
 PR 09-SEP-1996; AU-002208.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Hillon DJ, Metcalf D, Nicola NA, Willson T, Zhang JS;
 PI WPI; 97-259018/23.
 DR N-PSDB; T66164.
 PT DNA encoding animal haemopoietin receptor which interacts with
 PT interleukin-13 - useful to treat asthma, allergy or condition
 PT exacerbated by Ige production
 PS Claim 5; Page 48-50; 93pp; English.
 CC Novel mouse and human haemopoietin receptors (W09821 and W09822),
 CC designated NR4, comprise the interleukin-13 (IL-13) receptor
 CC alpha-chain. The mouse NR4 amino acid sequence was deduced from
 CC a composite DNA sequence (T66164) derived from genomic and cDNA
 CC clones. Recombinant NR4, or fusion proteins including NR4, can
 CC be produced in transformed host cells. The receptor molecules and
 CC their components are useful in the development of a range of
 CC agonists, antagonists, therapeutics and diagnostic reagents based
 CC on ligand interaction with its receptor, esp. for the development
 CC of cabs. capable of modulating the activity of IL-13 and related
 CC cytokines such as interleukin-4 for the treatment of allergy, asthma
 CC and other conditions relating to Ige.
 SQ Sequence 426 AA;

Query Match 73.5%; Score 1708.5; DB 1; Length 426;
 Best Local Similarity 74.9%; Pred. No. 8.9e-153;
 Matches 319; Conservative 40; Mismatches 66; Indels 1; Gaps 1;

QY 1 MEMPARLGLWALLLCAGGGGGGGAAPETPTPPVNLISVENLCTIVMTNPPEGASS 60
 DB 1 MARPALLGELLVLLMTATVAGVAAA-TEVQPVNTLSVENLCTIIMWSPPEGASP 59
 QY 1 NCSLWYSHHGDKDKKIAPETRSIEVPLNERICLOVSGSCSNESKPSILVEKCSIP 120
 DB 60 NCLTRYSHEDQDDKIIAPETHRKEELPLEDKICLOVSGSCSNESKPSILVEKCSIP 119
 QY 121 PEGDESAVTELOCIIMNLSYMKCSMLPGRTSPDTNTLYVMHRSLEKIQCNIFREG 180
 DB 120 PEGDESAVTELOCIIMNLSYMKCSMLPGRTSPDTNTLYVMHRSLEKIQCNIFREG 179
 QY 181 QYFGCSFDLTKVKSSEQHSVQIMVKNACKIRSFENIVPLTSRVKRPDPHINKLSFNH 240
 DB 180 QHICSFELTVEPXSFEHQVQIMVKNACKIRPSCKIVSLTSYVKRDPHINKLILKN 239
 QY 241 DDLYVOMENPQNFISRCLEFYEVENNSQTEHNFVVOACENPEPERNENTSCFVNP 300
 DB 240 GALLVOMKNPNFNSRCLTYEVENNTQTDHRNMLEVEDCQNSSEDRNNEGSCQOLP 299
 QY 301 GVLDPDLTVAVIRKTNKLCYEDDKLMSMSQEMSIGKRNSTLYITMLLIVPIYAGAI 360
 DB 300 GVLDAVYTVAVIRKTNKLCYEDDKLMSMSQEMSIGKRNSTLYITMLLIVPIYAVAV 359
 QY 361 IVLLLYLKRKLIIFPPIDPGKIFKEMFGQNDLTHMKRYDIYERKQTEEDSVLIE 420
 DB 360 IILFFYLKRKLIIFPPIDPGKIFKEMFGQNDLTHMKRYDIYERKQTEEDSVLIE 419
 QY 421 NLKRAA 426
 DB 420 NLKRAA 425

RESULT 4
 W58987
 ID W58987 standard; Protein; 177 AA.
 AC W58987;
 DT 11-SEP-1998 (first entry)

DE Homo sapiens adult placenta clone DA136-11 encoded protein.
 KM adult; placenta; cDNA library; clone DA136-11; secreted protein
 KM autoimmune disease; anti-inflammatory; immune; stimulation
 KW suppression;
 OS Homo sapien;
 PN W09814576-A4;
 PR 09-APR-1998.
 PR 03-OCT-1997; U18007.
 PR 04-OCT-1996; US-726237.
 PA (GEMV) GENETICS INST INC.
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D,
 PI Racie LA, Spaulding V, Treacy M;
 PI WPI; 98-240082/21.
 DR N-PSDB; Y11622.
 PT Nucleic acids encoding novel secreted proteins - useful as, e.g.
 PT anti-inflammatory, immuno-stimulatory or suppressing agents
 F3 Disclosure; Page 81-82; 110pp; English.
 CC The sequence is that of a secreted protein encoded by
 CC an isolated polynucleotide which may be of use in the
 CC production of therapeutic compositions for treating or
 CC ameliorating a medical condition in a mammal. Such compositions
 CC may be used for, e.g. research purposes as markers for
 CC tissues, molecular weight markers for gels, primers or probes, for
 CC nutrition as carbon, nitrogen or carbohydrate source. They can also be
 CC used as a cytokine for cell proliferation and differentiation activity,
 CC as immune stimulants or suppressors, e.g. for viral, bacterial or fungal
 CC infections, for autoimmune diseases such as multiple sclerosis or
 CC systemic lupus erythematosus, to regulate haematopoiesis, for tissue
 CC growth, as an activator or inhibitor, or as a chemotactic or
 CC chemokine, haemostatic and thrombocytic, receptor/ligand,
 CC anti-inflammatory or tumour inhibitor agents.
 SQ Sequence 177 AA;

Query Match 40.5%; Score 942; DB 1; Length 177;
 Best Local Similarity 100.0%; Pred. No. 3.7e-81;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 MVKNACKIRPSFNIPLTSRVKRPDPHINKLSFHNDDLYVOMENPQNFISRCLEFYEVE 264
 DB 1 MVKNACKIRPSFNIPLTSRVKRPDPHINKLSFHNDDLYVOMENPQNFISRCLEFYEVE 60
 QY 265 NNSQTEHNFVVOACENPEPERNENTSCFVNPGLPDLTVAVIRKTNKLCYEDD 324
 DB 61 NNSQTEHNFVVOACENPEPERNENTSCFVNPGLPDLTVAVIRKTNKLCYEDD 120
 QY 325 KLSMSQEMSIGKRNSTLYITMLLIVPIYAGAIIVLLLYLKRKLIIFPPIDP 381
 DB 121 KLSMSQEMSIGKRNSTLYITMLLIVPIYAGAIIVLLLYLKRKLIIFPPIDP 177

RESULT 5
 R2221
 ID R2221 standard; Protein; 415 AA.
 AC R2221;
 DT 22-JUL-1992 (first entry)
 DE Sequence of interleukin 5 (IL-5) receptor with signal peptide.
 KI Autoimmune disorder; therapy; eosinophilia.
 OS mouse.
 PN EP-475746-A.
 PR 18-MAR-1992.
 PR 11-SEP-1991; 308309.
 PR 11-SEP-1990; JP-240638.
 PA (TAKA) TAKATSU K.
 PI Takatsu K, Tomimaga A, Takagi S, Morita Y;
 PI WPI; 92-050329/12.
 PT Human and murine interleukin-5 receptor and DNA encoding them -
 PT for treatment of auto-immune and eosinophilia conditions
 PT involving IL-5.
 PS Claim 7; Page 21-23; 65pp; English.
 CC The inventors claim: an isolated cDNA sequence encoding murine
 CC (secretory) interleukin-5 (IL-5) receptor, which is synthesised from
 CC murine early B cell mRNA; an isolated murine (secretory) IL-5


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DB 12 PPV-NFIKATGLAQLVLMHPDPOEDQBRHVDLEHYKINAPDEQDXTREKCVPL 70
OY 91 NERCLQVSGCCSTNESEKPSILVEKCSPEGPDESATVLOCIMHNL----- 140
DB 71 HEGFAASRILKSSHTTLLASSWVAELKAPGSGTSVTMLCTTHVSSHTLRPYO 130
OY 140 SYMCSMLPGNTSPDNTVLTWYHRSLEKIHOCENIFRE--GGYFGCSFDTLYKDSF 197
DB 131 VSLFCTHVGKADBDQYFLYIRFGVLT--KQEYSRDLNNTACMFRTINSNGF 188
OY 198 EOHVSQIWMXDNACKIKRSPENIVPLTSRKPPPHIKNSFHNDLYVOMENPON-FLSR 256
DB 189 EQLVHINGSKRAIKRPFQDLFSPALDQVNPRTVETIESNSLYQWEKPLSAFDPH 248
OY 257 CLFEVEVNSQTFTHVFTYQEAKECENPEREVENVENTSCWVGVLPTLNTVIRAKT 316
DB 249 CFENELKIYNTKNG-----HLOKEKRLANKRISKIDVSTY-----SIOVRAV 292
OY 317 NKLCEYEDDKLMSNMSOEMSISGRNSTLYITMLIVPIYVAGAILVLLYLKRLKII--- 374
DB 293 SSSPBMGR-WGMSQPIYVGERKS-LVEMHLIVLP---TACFVLLIFSLICRVCHM 347
OY 374 --IFPPIPDGKIFKENGFGQNDTLHWKXYDIYKQTEEDSVV 417
DB 348 TRLEPPVAPKRSNIKDL-----PVTEYKPSNETRIEVV 382

RESULT 8
ID W36616
AC W36616
DE 30-MAR-1998 (first entry)
DE Celebus macaque Zcytor2 protein.
KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
OS Macaque sp.
FH Key Location/Qualifiers
FT 1..372 /label=Zcytor2
FT 1..372 /note="partial protein sequence"
FT W09733913-A1.
PD 18-SEP-1997.
PD 12-MAR-1997: U04043.
PD 13-MAR-1996: US-013345.
PA (ZYMO) ZYMOGENETICS INC.
PI Barmgartner JM, Farrah TM, Foster DC, Grant FU,
PI Ohara PJ.
DR N-PSDB: T96784.
DR N-PSDB: 97-470820/43.
PT New nucleic acid encoding testis-specific cytokine receptor - useful
PT for identification of ligands or antagonists, potentially for use as
PT male contraceptives or for infertility treatment
PS Example 4: Page 56-57; 79pp; English.
CC This sequence represents a novel ligand-binding receptor, Zcytor2,
CC which shares homology with cytokine receptors and is isolated from
CC testis tissue obtained from a Celebus macaque. The resulting polypeptide
CC is a receptor for cytokines (particularly interleukin-13) and is
CC expressed on the surface of testicular cells, probably being involved in
CC spermatogenesis. It can be used to detect ligands promoting proliferation
CC and/or differentiation of such cells in cultures and may also be used to
CC treat infertility. Antagonists of this receptor may be used to
CC characterise ligand-receptor interactions and as male-specific
CC contraceptives. By blocking the action of IL-13, receptor antagonists and
CC ligand-binding this receptor can also be used to modulate immune
CC function, e.g. in allergy and asthma, as a diagnostic to determine
CC circulating levels of ligand and also to isolate and purify ligands.
CC Antibodies can be used to assay circulating receptor (an abnormal level
CC may be indicative of disease such as cancer), for labelling cells that
CC express the receptor, and therapeutically as antagonist.
CC Sequence 372 AA;

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Query Match 13.0%; Score 302; DB 1; Length 372;
Best Local Similarity 27.5%; Pred. No. 2e-20;
Matches: 95; Conservative 60; Mismatches 127; Indels 64; Gaps 19;

OY 52 WNPPEGAS--NCSLWTFSHFGDKODKIAPEYRRSI-----EVLNERICLVGS 100
DB 53 WQPLSLDNKREKTEVEY-----ELKYNISSEETWITITNHLKDKDFDINKGIEAKIHT 107
OY 101 -----QCSNTESEKPSILVEK--ISPEGPDESATVLOCIMHNLMSYKMSWLPGRNTSP 154
DB 108 LIPWQC--TNGSEVSSVAELTWTIS--PQGLPEKVDQMDCVYIMQYLLCSMKPGISVLL 165
OY 155 DINTTLYWHSLEKIKHOCENIFRE--EGYFGCSFDTLYKDSFEOHVSQIWMXDNACKI 213
DB 166 DTNNLFTWYEGDLRALQCDYIKVDQNGRCRPY--LESSDVKDYICVNSSEETKPI 223
OY 214 KPSENIIVPLTSRKVPDPPIKNSFHNDLY--VOMENPONFI-SCLFEVEVNSQTF 269
DB 224 RSSYFTFQLOINIVKPLPPVC--LTCQESLYEIKLMSIFLGPAPCFYEIEIRDDDT 281
OY 270 ETHNVFTYQEAKECENPEREVENVENTS--CFMVPGVLPTLNTVIRIRVKTNKLCEYEDDKL 326
DB 282 T-----LVTTVENETTYTLKINETROLCFVY-----RSKVNITC-SDDG1 321
OY 327 WSNRQIM--SIGKRNSTLYITMLIVPIYVAGAILVLLYLKRL 370
DB 322 WSEMSDKQCMVEBELKTL--LFLPLP---GFLILVIFVTGL 361

RESULT 9
ID R25064
AC R25064
DE 10-DEC-1992 (first entry)
DE Human IL-5 receptor alpha chain.
KW Interleukin-5; chronic asthma; eosinophilia;
OS Homo sapiens.
FH Key Location/Qualifiers
FT 01-JUN-1992.
FT 06-DEC-1991: 120951.
FT 27-DEC-1990: EP-811030.
FT 30-APR-1991: EP-810327.
PA (HOEF) HOFMANN IA ROCHE & CO AG F.
PI Devos R, Fiers W, Plaetnick G, Tavernier J, Van Der Hayden J,
PI WPI: 32-218502/27.
DR N-PSDB: Q25790.
PT Recombinant alpha chain of human Interleukin-5 receptor - and DNA
PT encoding it, for treatment of Interleukin-5 mediated disorders
PT such as chronic asthma
PS Claim 7: Fig 1: 15pp; English.
CC This amino acid sequence was deduced from the nucleotide sequence,
CC revealed as detailed in Q25790. The cytoplasmic domain is 58 amino
CC acids long. A domain implicated in signal transduction processes
CC can not be found in this short cytoplasmic tail. Recombinant IL-5
CC alpha chain can be used as an IL-5 antagonist in chronic asthma or
CC other disease states with demonstrated eosinophilia. It may also be
CC used either alone or with the beta chain of the whole IL-5 receptor
CC as a tool for screening for IL-5 antagonists. See also Q25790-2, R25063.
CC Sequence 421 AA;

Query Match 12.8%; Score 296.5; DB 1; Length 421;
Best Local Similarity 24.8%; Pred. No. 8.1e-20;
Matches 102; Conservative 65; Mismatches 180; Indels 65; Gaps 16;

OY 33 PVTNLSVSTENICTVITWNP--PEGASSNCSLWTFSHFGDKODKIAPEYRRSIEVPLN 91
DB 32 PPV-NFIKATGLAQLVLMHPDPOEDQBRHVDLEHYKINAPDEQDXTREKCVPL 82
OY 92 ERICLOV-----GSQCSNTESEKPSILVEKCS--PEGPDESATVLOCIMHNL--- 140
DB 83 ESKCVTILKGFSAVRIILQNDHSHLASSWVAELKAPGSGTSVTMLCTTHVSSHTLRPYO 142

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QY 140 -----SY-----MRCSWLPGRTSPDTNTLYLWHRSLKIHQCENIFRE--GOYFGCSFDL 189
 DB 143 YSRRLRYQVSLHCTWLVGTDAPEDTQYFLYKRGSWTE--ECQESDITLGRINACFR 200
 QY 190 TKVKDSEFQHSVOIMVKNAGIKRSENIIVPLTSRYKPPPHIKNISFHNDDLYOWEN 249
 DB 201 TFLISGRDMLSVLVNSSSKHSAIRPFDQJFALHAIQINPPLNVAPEIGSTRLSIOWEK 260
 QY 250 PQR-FISRCLEFEVENNSQTEETHNFFVQEAECNEFERENNTSCFENVPGLPTLN 308
 DB 261 PVSAPFPHCDYEVKTHNTNG-----YDQIEKLTNAFISIIDLSKY----- 305
 QY 309 TVRIRVTKNLCEYEDKLSMWSQEMSGIKRRNSTLYITMLLIPVAVAGIIVLLYK 368
 DB 305 DVGVRVAVSSMCREAG-LMSEWSQPIYVGNDEHKPLNEMFVIYIMATICFILLISLICK 363
 QY 369 --RLKIIIPPIPDGKIFKEMFGDONDTLHMKKKIDYKQTKRETDSVVL 418
 DB 364 ICHLMWIKLFPPIDAPKSNIKDLFVTTN-----YKAGSSSETEIEVI 404

RESULT 10
 W35295
 ID W35295 standard; Protein; 380 AA.
 AC W35295;
 DT 27-MAR-1998 (first entry)
 DE Human IL-13 binding chain of the IL-13 receptor.
 KW Interleukin-13; IL-13; Interleukin-13 receptor binding chain; IL-13bc;
 KM mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
 OS allergy; asthma; immune complex disorder.
 OS Homo sapiens.
 FT FT Peptide
 FT FT Location/Qualifiers
 FT FT 1..25
 FT FT /label= signal_sequence
 FT FT /note= "putative"
 FT FT 26..380
 FT FT /label= mature_protein
 FT FT 26..341
 FT FT /label= extracellular_domain
 FT FT 342..362
 FT FT /label= transmembrane_domain
 FT FT 363..380
 FT FT /label= intracellular_domain
 FT FT Domain
 PN WO9731946-A1.
 PD 04-SEP-1997.
 PE 28-FEB-1997; U03124.
 PR 01-MAR-1996; US-609572.
 PA (GENE) GENETICS INST INC.
 PI Collins M, Donaldson D, Filz L, Neben T, Whiters M,
 PI Wood C;
 PI WPI: 97-448632/41.
 DR N-PSDB: T95214.
 PT New nucleic acid encoding interleukin-13 receptor binding chain and
 PT transformed cells - proteins, antibodies and inhibitors, for
 PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,
 PT and in diagnosis
 PS Claim 11; Pages 34-35; 49pp; English.
 CC The present sequence represents the human interleukin-13 (IL-13) binding
 CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
 CC mediator of the known biological activities of IL-13. Recombinant
 CC IL-13bc proteins, and antibodies raised against them, are used to
 CC inhibit the binding of IL-13 to its receptor. They are particularly used
 CC to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
 CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
 CC They are also used to treat immune deficiency (particularly in
 CC haematopoietic progenitor cells), cancer etc., and to increase macrophage
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
 CC with such activity is combined with IL-13bc and the mixture applied,
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor
 CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect
 CC expression of IL-13, its receptor or binding chain, and to raise specific
 CC antibodies which may be useful for treating some tumours.

SQ Sequence 380 AA.
 Query Match 12.7%; Score 295.5; DB 1; Length 380;
 Best Local Similarity 26.0%; Pred. No. 8; 6e-20;
 Matches 107; Conservative 63; Mismatches 169; Indels 73; Gaps 20;

QY 10 LVALILCAGGGGGGGAAPETPTNTNLSVENICTYIWMNPREGAS--SNCSLMWF 67
 DB 11 LVYFLISTFTGCGSSSDTEIKVNPDPDEFIVDPGYGLYGLQWQPLSLDHRKECTVEV- 70
 QY 68 SHEGKQDKKIAPETRRSI-----EVLNERICLOVGS---QCSNSEKPSILY 114
 DB 70 ---ELKYNIGSETKTIITIKNLHYKDGFDLNKGEAKIRHLLPQC-TNCEVQSSWA 124
 QY 115 EHC--ISPEGPDESATVTELOCIMHNLSTYMKCSWLPGRNTSPDTNTLYLWHRSLKIQ 172
 DB 125 ETTYWTS-PQGIPEIKVQMDCVYIMWQYLCSMKFQIGVLLDTNINLFTWEGDLHALQ 183
 QY 173 C-ENIREGOYEGCSFDLTKVSDSEFQHSVOIMVKNAGIKRSENIIVPLTSRYKPPDP 231
 DB 184 CVDYIKADQGNIGCRFPYLEASD--YKDFYICVNSSENKPIRSSYFTQLQNIYKPLPP 241
 QY 232 HIKNLSFHNDD--DLVQENPQNTI--SRCLPYEVEVANSQTEETHNFFVQEAECENPEF 287
 DB 242 --VYLFRESSECEIKLMSIPLGPPIPARCFYEIEIRDDYT-----LVATVENERY 293
 QY 288 ERNVENTS---CFMVGVLPLDNLTVIRIRVKNKLCYEDDKLSMWSQEM-----SIGRK 339
 DB 294 TLKTTNETHQLCFV-----RSKVNITC-SDDGIMSENSDQCEGEDLSKK 339

QY 340 RNSTLYITMLLIPVAVAGIIVLLYKRLKIIIFPPIDPGKIFKEMFGD 391
 DB 340 TLRFPLPF-----GFILLIVFTVGL--LKRKPTVY-KMIPERFCD 379

RESULT 11
 W35613
 ID W35613 standard; Protein; 380 AA.
 AC W35613;
 DT 30-MAR-1998 (first entry)
 DE Human Zcytor2 cytokine receptor protein.
 KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
 KW infertility; antagonist; contraceptive; diagnostic; therapeutic.
 OS Homo sapiens.
 FT FT Key
 FT FT Location/Qualifiers
 FT FT 340..363
 FT FT /label= transmembrane_domain
 FT FT 364..380
 FT FT /label= intracellular_domain
 FT FT 25..339
 FT FT /label= ligand_binding_domain
 FT FT Domain
 PN WO9733913-A1.
 PD 18-SEP-1997.
 PE 12-MAR-1997; U04043.
 PR 13-MAR-1996; US-013345.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Baumgartner JW, Farrah TM, Foster DC, Grant FJ,
 PI Ohara PJ;
 PI WPI: 97-470820/43.
 DR N-PSDB: T96782.
 PT New nucleic acid encoding testis-specific cytokine receptor - useful
 PT for identification of ligands or antagonists, potentially for use as
 PT male contraceptives or for infertility treatment
 PS Claim 2; Page 47-48; 79pp; English.
 CC This sequence represents a novel ligand-binding receptor. Zcytor2,
 CC which shares homology with cytokine receptors and was isolated from human
 CC placental polyA+ RNA. The resulting polypeptide is a receptor for
 CC cytokines (particularly interleukin-13) and is expressed on the surface
 CC of testicular cells, probably being involved in spermatogenesis. It can
 CC be used to detect ligands that promote proliferation and/or
 CC differentiation of such cells in cultures and may also be used to treat
 CC infertility. Antagonists of this receptor may be used to characterise

PR 12-JUN-1996; US-017843.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI (SMIR) SMITHKLINE BEECHAM CORP.
 DR Appelbaum ER, Hu J.
 WI: 98-052309/05.
 DR N-PSDB: V02295.
 PT DNA encoding human cytokine-peptide hormone receptor - useful for
 PT treating preventing or diagnosing, e.g. lowered resistance to
 PT infection, asthma, allergy, or haematopoietic disease
 PS Claim 15: Fig 1: 75pp: English.
 CC The sequence is that of the human cytokine/peptide hormone receptor
 CC (HR-1 receptor). This, or it's activators or agonists, can be used to
 CC treat, prevent or diagnose predisposition to lowered resistance to
 CC infection, asthma, allergic or haematopoietic disorders, e.g. where
 CC induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia,
 CC neutropenia or cytotoxic treatments for cancer. Antagonists of the
 CC receptor, e.g. antibodies or fragments of it may be used to treat
 CC conditions associated with overexpression of the HR-1 receptor, e.g.
 CC those listed above. Antibodies may also be used to assay levels of HR-1
 CC immunosays; to isolate and identify HR-1 receptor-expressing cells; or
 CC for affinity purification of the HR-1 receptor.
 SQ Sequence 380 AA:

Query Match 12.7% Score 295.5; DB 1; Length 380;
 Best Local Similarity 26.0%; Pred. No. 8.6e-20;
 Matches 107; Conservative 63; Mismatches 169; Indels 73; Gaps 20;

QY 10 LMALLCAGGGGGGGAAPETPTPTNLVSVENLCTVITWNPPEGAS--SNCSLMYF 67
 DB 11 LYTFLISTFCTSSSDTEIKVNPPOFEIYDGLYGLVQLQMPPLSLDHFECTVEY- 70
 QY 68 SHFGDKOPKRIAPFRRSI-----EVLNERICLOVGS-----QCSNTESEKPSILV 114
 DB 70 -----ELKRNIGSETWTKITITKLNHYDGDPLNKGIEAKIHTLLPQC--TNGSEVOSSWA 124
 QY 115 EKC--ISPPEGDSAVTELOCIMHNLVYKCSMLPGRNTSPDNTLYYHRSLEKIQ 172
 DB 125 ETTYWIS--PGIPEETKYQDMDCVYNNQYLLCSMKRPGIGVLDLTNNLEFWYEGDLHALQ 183
 QY 173 C-ENIFREGGYFGCSPLDKVKKSSFEQHSVQVMKDNAGKIRPSFNIVPLTSRYKPPDP 231
 DB 184 CVDYIRKADGONICGRPYLEASD--YKDEYICVNGSSENKPIRSSYFFPOLQNIYKPLP 241
 QY 232 HIKNLSFHDND--DLYVWENPQNF1-SRCLFEYEVVNSQFTHNIVFYQAKCENPEF 287
 DB 242 --VLLFTFRSSCEIKLMSIPLGPIPARCFYEIFEIRDIT-----LVATVENEY 293
 QY 288 ERNVENTS---CMVPGVLPDLNTVIRVKTNKLCEYEDDKLMSNMSQEM-----SIGKK 339
 DB 294 TLKTTNETROLQDEVV-----RSKVNICY-SDDGIWSEMSDKQCEGEDLSKK 339
 QY 340 RNSTLYITMLIVPVVAGAIIVLLYLKRLKIIFPPIPDGKIFKMGFD 391
 DB 340 TLLEWLP-----GFIILIVFYVGL--LKRKNYTP-KMIPBEFCD 379

RESULT 14
 ID W24972
 AC W24972;
 DT 22-JUN-1998 (first entry)
 DE Human Interleukin-13 beta receptor.
 KW Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.
 OS Homo sapiens.
 PN W09720926-A1.
 FD 12-JUN-1997.
 PF 07-NOV-1996; F01756.
 PR 06-DEC-1995; FR-014424.
 PA (SMIR) SANOFI SA.
 PI Caput D, Ferrara P, Laurent P, Vita N;
 DR WPI: 97-319773/29.

DR N-PSDB: T85826, T86464.
 PT New purified human interleukin-13 receptors - and related nucleic
 PT acids, useful for diagnosis and treatment of inflammation, allergy,
 PT etc.
 PS Claim 1; Figure 2a; 83pp: French
 CC This sequence represents interleukin-13 (IL-13) beta receptor. The
 CC invention relates to new purified peptides comprising 380 or 427 amino
 CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380
 CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
 CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
 CC affinity, but acquires high affinity when associated with the IL-4
 CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
 CC diagnostic probes to identify aberrant synthesis or genetic anomalies
 CC such as loss of heterozygosity and rearrangements, or chromosomal
 CC anomalies. They are also used for production of recombinant IL-13R beta
 CC and alpha which can be used as IL-13 antagonists, specifically to
 CC regulate IL-13-induced responses for treatment of inflammation and
 CC allergy (blocking synthesis of IL-13R). Antibodies are used (in standard
 CC immunosays) to diagnose diseases associated with abnormal expression
 CC of IL-13 receptors; when coupled to a toxin also for treatment of
 CC overproduction of IL-13R. Cells that express IL-13R at the surface are
 CC used to identify ligands and modulators of IL-13R. Note: IL-13R beta
 CC is encoded by the nucleic acid sequence shown in Figure 2a in the
 CC specification (T86464), which is not the same as that shown in the
 CC sequence listing (T85828).
 SQ Sequence 380 AA:

Query Match 12.7% Score 295.5; DB 1; Length 380;
 Best Local Similarity 26.0%; Pred. No. 8.6e-20;
 Matches 107; Conservative 63; Mismatches 169; Indels 73; Gaps 20;

QY 10 LMALLCAGGGGGGGAAPETPTPTNLVSVENLCTVITWNPPEGAS--SNCSLMYF 67
 DB 11 LYTFLISTFCTSSSDTEIKVNPPOFEIYDGLYGLVQLQMPPLSLDHFECTVEY- 70
 QY 68 SHFGDKOPKRIAPFRRSI-----EVLNERICLOVGS-----QCSNTESEKPSILV 114
 DB 70 -----ELKRNIGSETWTKITITKLNHYDGDPLNKGIEAKIHTLLPQC--TNGSEVOSSWA 124
 QY 115 EKC--ISPPEGDSAVTELOCIMHNLVYKCSMLPGRNTSPDNTLYYHRSLEKIQ 172
 DB 125 ETTYWIS--PGIPEETKYQDMDCVYNNQYLLCSMKRPGIGVLDLTNNLEFWYEGDLHALQ 183
 QY 173 C-ENIFREGGYFGCSPLDKVKKSSFEQHSVQVMKDNAGKIRPSFNIVPLTSRYKPPDP 231
 DB 184 CVDYIRKADGONICGRPYLEASD--YKDEYICVNGSSENKPIRSSYFFPOLQNIYKPLP 241
 QY 232 HIKNLSFHDND--DLYVWENPQNF1-SRCLFEYEVVNSQFTHNIVFYQAKCENPEF 287
 DB 242 --VLLFTFRSSCEIKLMSIPLGPIPARCFYEIFEIRDIT-----LVATVENEY 293
 QY 288 ERNVENTS---CMVPGVLPDLNTVIRVKTNKLCEYEDDKLMSNMSQEM-----SIGKK 339
 DB 294 TLKTTNETROLQDEVV-----RSKVNICY-SDDGIWSEMSDKQCEGEDLSKK 339
 QY 340 RNSTLYITMLIVPVVAGAIIVLLYLKRLKIIFPPIPDGKIFKMGFD 391
 DB 340 TLLEWLP-----GFIILIVFYVGL--LKRKNYTP-KMIPBEFCD 379

RESULT 15
 ID W41520
 AC W41520;
 DT 22-JUN-1998 (first entry)
 DE Human HR-1 receptor.
 KW HR-1 receptor; human; cytokine; infection; asthma; allergy;
 KW haematopoietic disorder; tumour; therapy; diagnosis.
 OS Homo sapiens.
 FH Key
 FT Peptide 1..21
 Location/Qualifiers

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 19, 2000, 14:58:48 (Search time 71.05 seconds
(without alignments)
283.481 Million cell updates/sec

Title: US-09-077-817-4

Perfect score: 2324

Sequence: 1 MEMPARLCGLMALLCAGCG.....QFKERTDVLLENKKASQ 427

Scoring table: BLOSUM62

Searched: 142080 seqs, 47169319 residues

Database: PIR_62.*

Word size: 0

Number of hits that pass the threshold: 142080

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 318 | 13.7 | 415 | 2 | SI2357 |
| 2 | 294.5 | 12.7 | 420 | 2 | SI21052 |
| 3 | 283.5 | 12.2 | 356 | 2 | SI21050 |
| 4 | 230 | 9.9 | 333 | 2 | SI21053 |
| 5 | 229 | 9.9 | 335 | 2 | SI21053 |
| 6 | 228 | 9.8 | 400 | 2 | SI21053 |
| 7 | 207 | 8.9 | 373 | 2 | SI21053 |
| 8 | 205.5 | 8.8 | 368 | 2 | SI21053 |
| 9 | 202 | 8.7 | 369 | 2 | SI21053 |
| 10 | 197.5 | 8.5 | 361 | 2 | SI21053 |
| 11 | 190 | 8.2 | 610 | 2 | SI21053 |
| 12 | 189 | 8.1 | 610 | 2 | SI21053 |
| 13 | 189 | 8.1 | 412 | 2 | SI21053 |
| 14 | 189 | 8.1 | 310 | 2 | SI21053 |
| 15 | 186 | 8.0 | 351 | 2 | SI21053 |
| 16 | 185 | 8.0 | 616 | 2 | SI21053 |
| 17 | 183 | 7.9 | 292 | 2 | SI21053 |
| 18 | 180 | 7.7 | 303 | 2 | SI21053 |
| 19 | 180 | 7.7 | 608 | 2 | SI21053 |
| 20 | 176 | 7.6 | 630 | 2 | SI21053 |
| 21 | 173 | 7.4 | 918 | 2 | SI21053 |
| 22 | 172.5 | 7.4 | 622 | 2 | SI21053 |
| 23 | 170 | 7.3 | 897 | 1 | SI21053 |
| 24 | 168 | 7.2 | 396 | 2 | SI21053 |
| 25 | 163 | 7.0 | 830 | 2 | SI21053 |
| 26 | 162.5 | 7.0 | 333 | 2 | SI21053 |
| 27 | 161.5 | 6.9 | 1092 | 2 | SI21053 |
| 28 | 161.5 | 6.9 | 719 | 2 | SI21053 |
| 29 | 158 | 6.8 | 378 | 2 | SI21053 |
| 30 | 157 | 6.8 | 896 | 1 | SI21053 |
| 31 | 156.5 | 6.7 | 378 | 2 | SI21053 |
| 32 | 154.5 | 6.6 | 896 | 1 | SI21053 |
| 33 | 149 | 6.4 | 878 | 1 | SI21053 |
| 34 | 146.5 | 6.3 | 608 | 2 | SI21053 |
| 35 | 145 | 6.2 | 638 | 2 | SI21053 |

| | | | | | | |
|----|-------|-----|------|---|---------|--------------------|
| 36 | 145 | 6.2 | 638 | 2 | SI21053 | somatotropin recep |
| 37 | 144.5 | 6.2 | 1097 | 2 | SI21053 | leukemia inhibitor |
| 38 | 144 | 6.2 | 918 | 2 | SI21053 | interleukin-6 sign |
| 39 | 142.5 | 6.1 | 917 | 2 | SI21053 | glycoprotein 130 |
| 40 | 141 | 6.1 | 638 | 2 | SI21053 | somatotropin recep |
| 41 | 140 | 6.0 | 638 | 2 | SI21053 | somatotropin recep |
| 42 | 139 | 6.0 | 508 | 1 | SI21053 | erythropoietin rec |
| 43 | 139 | 6.0 | 634 | 2 | SI21053 | somatotropin recep |
| 44 | 135.5 | 5.8 | 286 | 2 | SI21053 | granulocyte-macrop |
| 45 | 134.5 | 5.8 | 557 | 2 | SI21053 | interferon alpha I |

ALIGNMENTS

RESULT 1
SI2357
Interleukin-5 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Mar-1998
C:Accession: SI2357
R:Takaki, S.; Tomimaga, A.; Hiroshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu
OMBO J. 9, 4367-4374, 1990
H>Title: Molecular cloning and expression of the murine interleukin-5 receptor.
H:Reference number: SI2357, PMID:91092260
H:Accession: SI2357
H>Status: preliminary
H:Molecule type: mRNA
A:Residues: 1-415 <TRAK>
A:Cross-references: GB:ID0205; NID:q220465; PID:d1014936; PID:q220466
C:Keywords: cytokine receptor; transmembrane protein

Query Match 13.7% Score 318; DB 2; Length 415;
Best Local Similarity 23.9%; Pred. No. 1.6e-17;
Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;

QY 33 PPTVNLSSVENICTVMTWNP-PEGASSNCSLWFSHF-GDKDKKIAPETRSIEVPL 90
DB 29 PPTVNLSSVENICTVMTWNP-PEGASSNCSLWFSHF-GDKDKKIAPETRSIEVPL 90
QY 91 NERICLQVSGSCSTNESEKPSILVEKICSPEDDPESAVTELQCIWHNL----- 140
DB 88 HEGFAASVRLTKSSHTLSSWSVSAELKAPGSPGTSVNLCTHTTVSSHTLRPYQ 147
QY 140 SYMKCSWLPGRNTSPDTNITLYTHNSLEKIHOCENTFRF--GQYECSDLTAKVDSF 137
DB 148 VSLRCTLVGGKADPEDTQYLYRFGVLE--KCOEYSRDLNRRNTACWPFRTFINSKGF 205
QY 198 EOHVSQVTHVDMNGKIKPSPNIYPLTSRVKPDPPHKNLSFHHNDLTVQKRNQNF-FISR 256
DB 206 EQLVTHVDMNGKIKPSPNIYPLTSRVKPDPPHKNLSFHHNDLTVQKRNQNF-FISR 256
QY 257 CLPEYEVNNSQTEHNHFVVOEAKCENPEERNEVENTSCFVAPGVLPDLTVIRIKVT 316
DB 266 CFVPEYEVNNSQTEHNHFVVOEAKCENPEERNEVENTSCFVAPGVLPDLTVIRIKVT 316
QY 317 NKLCYEDDKLMSWSQMSGKRRNSTLYTTLIYVYAGAILVLLYLAKRKII--- 374
DB 310 SSSCPRMGR-WGEMSOPIYVGERKRS-LVEMHIVLP---TAACFVLLIRSLICRCHLV 364
QY 374 --TFPPIDPGKIFKEMFGQNDLHWKVDYKQTEKETSQV 417
DB 365 TRLEPPVAPKSNIKDL-----PVTEYERKSNETKIEVV 399

RESULT 2
SI21052
Interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Feb-1998
C:Accession: SI21052; A46175
R:Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tomimaga, A.; Takatsu, K.

Query Match 9.9%: Score 230; DB 2; Length 333;
 Best Local Similarity 24.8%; Pred. No. 9.6e-11;
 Matches 82; Conservative 51; Mismatches 145; Indels 52; Gaps 14;

```

OY 33 PPTNLVSVENLCTVITWNP-PEGASSNCSLMYFSGDKODKIAPETRRSIEVPLN 91
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 32 PPV-NFTIKYGLAQLVLOMKPNPDQEGRNINLEY-----QYKINAPK-EDDYETRIT 82
OY 92 ERICLOV-----GSGCSTNESEKPSILVEKIS----PPGDPESATVLELOCIMHNL--- 140
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 83 ESKCVTLHKGFSAVRITLONDSHLASSWASALHAPSPSGTSVNLCTTNTEDN 142
OY 140 -----SY-----MKCSMLPGRNTSPDTNYTLYYMHSLEKIHOCENIFRE--GOYFGCSFDL 189
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 143 YSRLRISQVSLHCTWLTGDAPEDTQYFLYRGSWTE--ECQESKDTLGRNACWEP 200
OY 190 TKVDSSEFQHSVOIMKDNAGKIKPSENIPLTSRYKPPDPHINKLSFHNDLYQWEN 249
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 201 TFLSKGRDWLAVLVNGSSKSHAIRPQDLFALHAIQINPLVNTAEIEGTRLSIQWEK 260
OY 250 PQN-FISRCLEFYEYVNNNSQFETHNVFYQAKCENPEFERNVENTSCFMPVGLPTDILN 308
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 261 PVSAFPIHCEDEYKLNHTNRG-----YLQLEKLTMTAFISIIDLSKY----- 305
OY 309 TVRIKVTNKLCEYEDDKLMSNMSEMSIGK 338
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 305 DVQYRAVSSMCREAG-LMSEMSQPIYGVK 333
  
```

RESULT 5

A:Accession: A40267
 A:Species: Homo sapiens (man)
 C:Date: 17-Jan-1992 #sequence, revision 17-Jan-1992 #text, change 10-Sep-1997
 C:Accession: A40267
 R: Tavernier, J.; Devos, R.; Cornelis, S.; Tuyen, T.; Van der Heyden, J.; Fiers, W.; Pl
 Cell 66, 1175-1184, 1991
 A:Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-spec
 A:Reference number: A40267; MUID:92005669
 A:Accession: A40267
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-335 <TRAV>
 A:Cross-references: GB:M75914; NID:9186387; PID:9186388
 C:Keywords: cytokine receptor; transmembrane protein

Query Match 9.9%: Score 229; DB 2; Length 335;
 Best Local Similarity 24.7%; Pred. No. 1.2e-10;
 Matches 82; Conservative 51; Mismatches 147; Indels 52; Gaps 14;

```

OY 33 PPTNLVSVENLCTVITWNP-PEGASSNCSLMYFSGDKODKIAPETRRSIEVPLN 91
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 32 PPV-NFTIKYGLAQLVLOMKPNPDQEGRNINLEY-----QYKINAPK-EDDYETRIT 82
OY 92 ERICLOV-----GSGCSTNESEKPSILVEKIS----PPGDPESATVLELOCIMHNL--- 140
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 83 ESKCVTLHKGFSAVRITLONDSHLASSWASALHAPSPSGTSVNLCTTNTEDN 142
OY 140 -----SY-----MKCSMLPGRNTSPDTNYTLYYMHSLEKIHOCENIFRE--GOYFGCSFDL 189
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 143 YSRLRISQVSLHCTWLTGDAPEDTQYFLYRGSWTE--ECQESKDTLGRNACWEP 200
OY 190 TKVDSSEFQHSVOIMKDNAGKIKPSENIPLTSRYKPPDPHINKLSFHNDLYQWEN 249
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 201 TFLSKGRDWLAVLVNGSSKSHAIRPQDLFALHAIQINPLVNTAEIEGTRLSIQWEK 260
OY 250 PQN-FISRCLEFYEYVNNNSQFETHNVFYQAKCENPEFERNVENTSCFMPVGLPTDILN 308
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 261 PVSAFPIHCEDEYKLNHTNRG-----YLQLEKLTMTAFISIIDLSKY----- 305
  
```

OY 309 TVRIKVTNKLCEYEDDKLMSNMSEMSIGKRR 340
 DB 305 DVQYRAVSSMCREAG-LMSEMSQPIYGVFSR 335

RESULT 6

A:Accession: A41286
 A:Species: Homo sapiens (man)
 C:Date: 22-Jan-1993 #sequence, revision 22-Jan-1993 #text, change 12-Jun-1998
 C:Accession: S06945; A41286; A4474
 R: Gearing, D.P.; King, J.A.; Gough, N.M.; Nicola, N.A.
 A:Title: Expression cloning of a receptor for human granulocyte-macrophage colony-sti
 A:Reference number: S06944; MUID:90059966
 A:Accession: S06945
 A:Molecule type: mRNA
 A:Residues: 1-430 <GEAS>
 A:Cross-references: EMBL:X17648; NID:932087; PID:932089
 R: Crossler, K.S.; Wong, G.G.; Mathew-Prevot, B.; Nathan, D.G.; Sieff, C.A.
 Proc. Natl. Acad. Sci. U.S.A. 88, 7744-7748, 1991
 A:Title: A functional isoform of the human granulocyte/macrophage colony-stimulating
 A:Reference number: A41286; MUID:91352066
 A:Accession: A41286
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 347-400 <CRO>
 R: Apple, G.; Wallson, T.A.; Henke, A.; Gough, N.M.
 Genomics 14, 455-461, 1992
 A:Title: Arrangement and localization of the human GM-CSF receptor alpha chain gene C
 A:Reference number: A4474; MUID:93052350
 A:Accession: A4474
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-377-400 <RAP>
 A:Cross-references: GB:S48539; NID:9258858; PID:9258859
 A:Note: sequence extracted from NCBI backbone (NCBI:P117980)
 C:Genetics:
 A:Gene: GDB:CSF2RA; CSF2R
 A:Cross-references: GDB:118777; OMIM:306250; OMIM:425000
 A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
 C:Keywords: glycoprotein; growth factor receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-400/Product: granulocyte-macrophage colony-stimulating factor receptor #status p
 F:322-346/Domain: transmembrane #status predicted <TM>
 F:46,54,99,123,182,195,223,229,272,305/Binding site: carbohydrate (Asn) (covalent

Query Match 9.8%: Score 228; DB 2; Length 400;
 Best Local Similarity 22.4%; Pred. No. 1.7e-10;
 Matches 90; Conservative 82; Mismatches 180; Indels 50; Gaps 18;

```

OY 31 TOPPTNLVSVENLCTVITWNPPEGAS--SNCSLMYFSGDKODKIAPETRRSIEV 89
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 29 TVAPASSLNVAFDR-TMNLMSDQENTFTSKPL-----TDKKNVVEPRLSNNECSC 81
OY 90 LNERCYQVSGCSTNSEKPSILVEKISPPGDPESATVLELOCIMHNLSTYKMSLPG 149
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 82 TFRFICHEGTEFVAVHTNSQRFQRLYPNSREGTAONFSCFYNDLNMCTWARG 141
OY 150 RNTSPDTNYTLYYMHSLEKIHOCENIFRE--GOYFGCSFD-LTKVDSSEFQHSQVLMVK 207
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 142 PTPARPDYQFLYITNSKRREIRCPYIQQSGTHVGHGCHLNLSTLSRNY-----FLVN 195
OY 208 DNACIKPSE--NIVPLTSRYKPPDPHINKLSFHNDLYQWENPQNF--ISRCLEF-YEV 262
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 136 GTSSEIQFEDSLDTRKIERPNSNVTYRCVTHCLVAKWQPRYQKSLYDFQYOL 255
OY 263 EVN--NSQFETHNVFYQAKCENPEFERNVENTSCFMPVGLPTDILNTYRIKTKKLC 320
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 256 DVHRKNTQPTENLILNVSGDENR-----YNFSSSEPRAKHSVIRADAVRIL 304
  
```

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-369 <RE>
A:Cross-references: GB:I20048; NID:g404067; PIDN:AAA39286.1; PID:g404068
R:Kimaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
Biochem. Biophys. Res. Commun. 193, 356-363, 1993
A:Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of f
A:Reference number: JN0592; MUID:93277575
A:Accession: JN0592
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-369 <KU>
A:Cross-references: DDBJ:I31565; NID:g303684; PIDN:BA02760.1; PID:d1003265; PID:g30303684
R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
A:Reference number: JN0775; MUID:93366191
A:Accession: JN0775
A:Molecule type: mRNA
A:Residues: 1-369 <KO>
A:Cross-references: GB:I33821; NID:g4336045; PIDN:BA02974.1; PID:d1003480; PID:g433604
R:Chiu, R.K.; Dougherty, G.J.
submitted to the EMBL Data Library, October 1993
A:Description: Regulation of CD44-mediated cellular adhesion by the IL-2 R gamma chain
A:Reference number: S37582
A:Accession: S37582

| | | | | | | | | | |
|---------|-----|--------------|-----|------------|------|--------|-----|------|-----|
| Matches | 76; | Conservative | 52; | Mismatches | 131; | Indels | 44; | Gaps | 14; |
|---------|-----|--------------|-----|------------|------|--------|-----|------|-----|

A:Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosome
A:Accession number: 153398; MIMD:95104285
A:Accession: 153398
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:575852; NID:g861554; PIDN:AAB32904.1; PID:g861555
C:Genetics:
A:Gene: IL-2Rgamma
A:Mutons: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
C:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), bet
eotors.
C:Function:
A:Description: receptor for interleukin-2
A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, N
C:Superfamily:..interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
F:1-122/Domain: signal sequence #status predicted <SIG>
F:12-365/Product: interleukin-2 receptor gamma chain #status predicted <KAT>
F:256-384/Domain: transmembrane #status predicted <TM>
F:71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predict

Best Local Similarity 24.0%; pred. No. 9.1e-09;
Matches 76; Conservative 63; Mismatches 121. Indels 57. Gaps 16.

103. SINESNP5LIVEAC1BPGEDESAVTELCIWNHLSYMKCSWLPGRNTSPD---TNYT 159

03 31 SANEDINADLELISIAPEHLSAPILPLPEVQCFVFNIEYMCIW----NSSSEQATNLT 86

```

02 100 LIWHRSELEHQCENTFRREGQYHGCSFDLTKVKDSSFEQHSVQ-----IMWKDNAGKI 213
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

0/ UNINAVSD - - - - - NNIFFECSHILFSKELT - - - - - SGCQIQKEDIQLYQTFVWQLOBPQKPPQ 139

[illegible]

196 ENLILSINLESQLELRMS-RHAKERCLQYLVOYRSNRDR

2 / 1 TUNNEL VERBODEN EN NIET TOEGELATEN -- I V R K R K T N K L C Y E D D K L W S 328

Db 197 SWT-----ELIVNEPRESLPSV--DELRKYFRVRSRYNPICGSSOO-WS 239

QY 329 NMSEMSIGK---KRNSTLITMLIIVPVIYAGAIIVLL---YLKRLKIIIFPPIDPG 382

Db 240 KMSOPVHMSHYEENSLEALVLPVGMGLITLIIYVCLWERN-----PIIP-PI 293

QY 383 KIFKEMFGDONDDTLHW 399

Db 294 KNLDELTEYOGNFSAN 310

RESULT 9

A:Accession: A42565
Interleukin-2 receptor gamma chain - human
C:Species: Homo sapiens (man)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1993
C:Accession: A42565; A46591; 154332
R:Takekoshi, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H.; Science 257, 379-382, 1992
A:Title: Cloning of the gamma chain of the human IL-2 receptor.
A:Reference number: A42565; M01D:92335883
A:Accession: A42565
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-369 <FAK>
A:Cross-references: GB:DJ1086; NID:q303611; PIDN:BA01857.1; PID:di002334; PID:g219890
A:Experimental source: MOLT beta lymphoid cells
A>Note: sequence extracted from NCBI database (NCBI:109167)
R:Moguchi, M.; Adelstein, S.; Gao, X.; Leonard, W.J.
J. Biol. Chem. 268, 13601-13608, 1993
A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.
A:Reference number: A46591; M01D:93293887
A:Accession: A46591
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:J12183; NID:q307056; PIDN:AA59145.1; PID:q307058
R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Wallard, H.F.; Hum. Mol. Genet. 2, 1099-1104, 1993
A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-linked
A:Reference number: I54332; M01D:94004847
A:Accession: I54332
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RE2>
A:Cross-references: GB:J19546; NID:q349631; PIDN:AAC37524.1; PID:q349632
C:Genetics: GDB:IL2RG; SCIDX1; IMD4
A:Cross-references: GDB:134807; OMIM:308380
A:Map position: Xq13.1-Xq13.1
A:Intons: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A>Note: defects are associated with an X-linked form of severe combined immunodeficiency
C:Superfamily: Interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunodeficiency

Query Match 8.7% Score 202; DB 2; Length 369;

Best Local Similarity 27.2% Pred. NO. 1.7e-08; Mismatches 101; Indels 48; Gaps 14;

Db 131 ELQCIWHLNLSYKCSWLPGRNTSPDNTLYLYWRSI--EKIHOCEN-IFREGQYFGCSF 187

Db 59 EVOCEYFVNEVMNCNTNMSSEPPQ-TNLTLHYWKNSDNDKQVCSHYLSEITSGC-- 116

QY 188 DLTKVDSSEFQHSVOQIMVNDNAGKIKPSFNIVPLTSRVAPDPPIHNLSEFH--NDLY 244

Db 116 QLOKKEHLVQTFVYOL--ODPREPRQATQMKLOLVIPMAV--DNLTLLKLSQSLE 171

QY 245 VQENPONTISRCI---FEVEYVNSQTFETHNVFYQEAKECEPEREVENVENTSCFMP 300

Db 172 LAMNN--RFLNHLCEHLVQRTMDHSHWT-----EQSVDRHAKFSLP 211

QY 301 GVLPTLNTVIRKVNKLCYEDDKLMSNMSQEMSIG--KRNSTLYITMLIIVPIVA 357

Db 212 SVESQKRYEVRNRSRNPCL-GSAQHWSEWSHPIMWSNNTSKENPFLFAEAVYISGSM 270

QY 353 GATVLL---LYLRLKIIIFPPIP 379

Db 271 GLIISLCVYFWLER---TMPRIIP 291

RESULT 10

A:Accession: J01655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 10-Sep-1997
C:Accession: J01655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.; Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA
A:Reference number: J01655; M01D:93075121
A:Accession: J01655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-references: DDBJ:DJ3154; NID:q222848; PID:di002939; PID:g222849
A:Experimental source: Kidney
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <Sig>
F:24-831/Product: prolactin receptor #status predicted <MAT>
F:439-462/Domain: transmembrane #status predicted <TM>
F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (cov

Query Match 8.5% Score 197.5; DB 2; Length 831;

Best Local Similarity 23.1% Pred. NO. 1.1e-07; Mismatches 91; Conservative 59; Mismatches 159; Indels 85; Gaps 19;

QY 32 QP--PTNLSVSVENLCTV--IWT-MNP--EGASSNCSIMYFSGDKODKRIAPETR 84

Db 126 QFGSPV-NLTLETKRSANIMYLMKMSPLADASSN---HLVHY---ELRIKPEKE 176

QY 85 SIENPLNERICLOVSGCNSNE-----SKRPSILVEKCSPP 121

Db 177 EWEI---ISVGVOYQCKNRLNAGMRVYVQRTIDPEGSEWSESRHLLPSSGSP 231

QY 122 EGDPEAVTELOCIMHLSYKCSWLPGRNTSPDNTLYLYWRSI-EKIHOCENIFREGQ 181

Db 232 F-----KPTIIKRSPEKKEFTCKMKRGDGHPTNTLLXSEGEQVYECED-YITAG 285

QY 183 YFGCSFDLTKVDSSEFQHSVOQIMVNDNAGKIKPSFNIVPLTSRVKDPD---HIKNT 236

Db 286 PMSCYFD--KKHSEFWITVIVRATNEMGSNSDPHYVDVTIYVCPDPVNVNLTLEKRP 343

QY 237 SFHNDLLYQENPONTISR---CLFEYEVVNSQTFETHNVFYQEAKECEPEREVENVE 292

Db 344 INRPVYVLTWSPPLADVSGMLTLEYELRLKPEESEEETFEVQ-QYQYKFSIN-- 401

QY 293 NTSCEWPGVLPPTLNTVIRKVNKLCYEDDKLMSNMSQEMSIGKRNSTLYITMLIIV 352

Db 401 -----PKKVIYIQHCKP-----DHRGWSMSSEENYQIPNDPRVADMIVIV 444

QY 353 PVIYAGAIIVLL---LYLRLKIIIF--PIIPDP 381

Db 445 LGVLSLILCLINSMWTMLVKGYRMTFTMLPVPGP 478

RESULT 11

A:Accession: A34631
lactogen receptor 1 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 10-Sep-1997
C:Accession: A34631
R:Zhang, R.; Buckzo, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.; Biochem. Biophys. Res. Commun. 168, 415-422, 1990
A:Title: Isolation and characterization of two novel rat ovarian lactogen receptor cD
A:Reference number: A34631; M01D:90241201

A:Accession: A34631
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-610 <ZNR>
 A:Cross-references: GB:M4083; NID:9205122; PID:9205123
 A:Note: the authors translated the codon GAG for residue 533 as G1Y

Query Match 8.2%; Score 190; DB 2; Length 610;
 Best Local Similarity 23.7%; Pred. No. 2.9e-07;
 Matches 68; Conservative 43; Mismatches 120; Indels 56; Gaps 10;

QY 109 KPSILVEKICSPEDPSAVTELOCIWNLSTYKCSMLPGRNTSPDNTLYLWHSLE 168
 DB 25 KPEI--HKCRSP---DKET-----FTCMWNPCTDGLPTNLSLYSKSGEK 65
 QY 169 KIHOCENIFREGOYFGCSFDLTKYKDSFEQHSQIWKKNAGKIKSFNIVPLTSVKP 228
 DB 66 TTYECPDYKTSQPN--SCFF--SKOYTSIMKIYIITVNATNOMGSSSDPLYVDVYIYEP 122
 QY 229 DPP-----HIKNLSFHNDDLYVOMENPQNFISR-----CLFEYEVNNSQTEHNVEFYOE 279
 DB 123 EPPNRLTLEVQOLKDKRTYLMVKMSPTIIDVKTGWTMEYELRKEEAEWEIHF--- 180
 QY 280 AKCENPEERVENTSCFMPGVLPTLNTVRIKVTNKLCEYEDDKLMSWQSEMSIGKK 339
 DB 180 -----TGHOIFKVFEDLYPGQKYLVOYR-----CKPDHGYSRMSQSSSEVEMP 222
 QY 340 RNSTLYTMLLIYVIVAGAILVLLYLKRLK-----IIFPPIPD 381
 DB 223 NDFLTKDTTWIITAILSAVICLIIMWAVALKGYSMTCTIFFPVPGP 269

RESULT 12

A36116
 Prolactin receptor 2 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 10-Sep-1997
 C:Accession: A36116
 R:Shiota, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boulton, J.M.; Edey, M.; Djiane, J.
 M.O. Endocrinol. 4, 1136-1143, 1990
 A:Title: Expression of two forms of prolactin receptor in rat ovary and liver.
 A:Reference number: A36116; MUID:91155946
 A:Accession: A36116
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-610 <SHI>
 A:Cross-references: GB:M57668; NID:9206366; PID:9206367; GB:M60728

Query Match 8.1%; Score 189; DB 2; Length 610;
 Best Local Similarity 23.7%; Pred. No. 3.4e-07;
 Matches 68; Conservative 43; Mismatches 120; Indels 56; Gaps 10;

QY 109 KPSILVEKICSPEDPSAVTELOCIWNLSTYKCSMLPGRNTSPDNTLYLWHSLE 168
 DB 25 KPEI--HKCRSP---DKET-----FTCMWNPCTDGLPTNLSLYSKSGEK 65
 QY 169 KIHOCENIFREGOYFGCSFDLTKYKDSFEQHSQIWKKNAGKIKSFNIVPLTSVKP 228
 DB 66 TTYECPDYKTSQPN--SCFF--SKOYTSIMKIYIITVNATNOMGSSSDPLYVDVYIYEP 122
 QY 229 DPP-----HIKNLSFHNDDLYVOMENPQNFISR-----CLFEYEVNNSQTEHNVEFYOE 279
 DB 123 EPPNRLTLEVQOLKDKRTYLMVKMSPTIIDVKTGWTMEYELRKEEAEWEIHF--- 180
 QY 280 AKCENPEERVENTSCFMPGVLPTLNTVRIKVTNKLCEYEDDKLMSWQSEMSIGKK 339
 DB 180 -----TGHOIFKVFEDLYPGQKYLVOYR-----CKPDHGYSRMSQSSSEVEMP 222
 QY 340 RNSTLYTMLLIYVIVAGAILVLLYLKRLK-----IIFPPIPD 381
 DB 223 NDFLTKDTTWIITAILSAVICLIIMWAVALKGYSMTCTIFFPVPGP 269

RESULT 13

A41070
 prolactin receptor NB2 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 10-Sep-1997
 C:Accession: A41070; 155417
 R:Ali, S.; Pellegrini, I.; Kelly, P.A.
 J. Biol. Chem. 266, 20110-20117, 1991
 A:Title: A prolactin-dependent immune cell line (NB2) expresses a mutant form of prolactin receptor.
 A:Reference number: A41070; MUID:92041834
 A:Accession: A41070
 A:Molecule type: mRNA
 A:Residues: 1-412 <ALI>
 A:Cross-references: GB:M74152; NID:9206389; PID:9206390
 R:O'Neal, K.D.; Yu-Lee, L.Y.
 J. Biol. Chem. 269, 26076-26082, 1994
 A:Title: Differential signal transduction of the short, NB2, and long prolactin receptor.
 A:Reference number: 155417; MUID:95014432
 A:Accession: 155417
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-412 <RES>
 A:Cross-references: EMBL:U07567; NID:9641963; PID:9641964
 A:Experimental source: NB2-11C cell line
 C:Keywords: transmembrane protein

Query Match 8.1%; Score 189; DB 2; Length 412;
 Best Local Similarity 23.7%; Pred. No. 2.1e-07;
 Matches 68; Conservative 43; Mismatches 120; Indels 56; Gaps 10;

QY 109 KPSILVEKICSPEDPSAVTELOCIWNLSTYKCSMLPGRNTSPDNTLYLWHSLE 168
 DB 25 KPEI--HKCRSP---DKET-----FTCMWNPCTDGLPTNLSLYSKSGEK 65
 QY 169 KIHOCENIFREGOYFGCSFDLTKYKDSFEQHSQIWKKNAGKIKSFNIVPLTSVKP 228
 DB 66 TTYECPDYKTSQPN--SCFF--SKOYTSIMKIYIITVNATNOMGSSSDPLYVDVYIYEP 122
 QY 229 DPP-----HIKNLSFHNDDLYVOMENPQNFISR-----CLFEYEVNNSQTEHNVEFYOE 279
 DB 123 EPPNRLTLEVQOLKDKRTYLMVKMSPTIIDVKTGWTMEYELRKEEAEWEIHF--- 180
 QY 280 AKCENPEERVENTSCFMPGVLPTLNTVRIKVTNKLCEYEDDKLMSWQSEMSIGKK 339
 DB 180 -----TGHOIFKVFEDLYPGQKYLVOYR-----CKPDHGYSRMSQSSSEVEMP 222
 QY 340 RNSTLYTMLLIYVIVAGAILVLLYLKRLK-----IIFPPIPD 381
 DB 223 NDFLTKDTTWIITAILSAVICLIIMWAVALKGYSMTCTIFFPVPGP 269

RESULT 14

A29884
 prolactin receptor precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 20-Mar-1998
 C:Accession: A29884
 R:Boulton, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edey, M.; Shiota, M.; Banville, J.
 Cell 55, 69-77, 1988
 A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth factor receptor family.
 A:Reference number: A29884; MUID:88165059
 A:Accession: A29884
 A:Molecule type: mRNA
 A:Residues: 1-310 <BOU>
 A:Cross-references: GB:M19304; NID:9206364; PID:9206365
 C:Keywords: transmembrane protein
 F:1-19/Domain: signal sequence
 F:20-310/Product: prolactin receptor #status predicted <SIG>
 F:20-310/Product: prolactin receptor #status predicted <MAR>

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 20, 2000, 06:19:55 ; Search time 35.05 Seconds
(without alignments)
354.343 Million cell updates/sec

Title: US-09-077-817-4

Sequence: 1 MEMPARLCGLNALLCAGCG.....QTKETDSVLIENIKKASQ 427

Scoring table: BLOSUM62

Searched: 80000 seqs, 29085965 residues

Database: SwissProt_38.*

Word size: 0

Number of hits that pass the threshold: 80000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|------------|---------------------|
| 1 | 2324 | 100.0 | 427 | 1131_HUMAN | P78552 homo sapien |
| 2 | 1698.5 | 73.1 | 424 | 1131_MOUSE | O09030 mus musculu |
| 3 | 318 | 13.7 | 415 | IL3R_MOUSE | P21183 mus musculu |
| 4 | 296.5 | 12.8 | 420 | IL3R_HUMAN | Q01344 homo sapien |
| 5 | 295.5 | 12.7 | 380 | 1132_HUMAN | Q14627 homo sapien |
| 6 | 228 | 9.8 | 400 | GMCR_HUMAN | P15509 homo sapien |
| 7 | 207 | 8.9 | 373 | CYRG_CANFA | P40321 canis famill |
| 8 | 205.5 | 8.8 | 369 | CYRG_MOUSE | P34302 mus musculu |
| 9 | 202 | 8.7 | 369 | CYRG_HUMAN | P31785 homo sapien |
| 10 | 198.5 | 8.5 | 831 | PRLR_MELGA | Q91094 meleagris g |
| 11 | 197.5 | 8.5 | 831 | PRLR_CHICK | Q04594 gallus gall |
| 12 | 197 | 8.5 | 379 | CYRG_BOVIN | O95118 bos taurus |
| 13 | 189 | 8.1 | 610 | PRLR_RAT | P05710 rattus norv |
| 14 | 186 | 8.0 | 581 | PRLR_BOVIN | Q28172 bos taurus |
| 15 | 185 | 8.0 | 616 | PRLR_RABIT | P14787 oryctolagus |
| 16 | 180 | 7.7 | 608 | PRLR_MOUSE | O08501 mus musculu |
| 17 | 176 | 7.6 | 630 | PRLR_ORENT | O91513 oreochromis |
| 18 | 173 | 7.4 | 918 | IL3B_HUMAN | P40189 homo sapien |
| 19 | 172.5 | 7.4 | 622 | PRLR_HUMAN | P16771 homo sapien |
| 20 | 168 | 7.2 | 897 | CYRB_HUMAN | P32927 homo sapien |
| 21 | 168 | 7.2 | 396 | IL3A_MOUSE | P26952 mus musculu |
| 22 | 163 | 7.0 | 830 | PRLR_COLLI | Q90374 columba liv |
| 23 | 162 | 7.0 | 581 | PRLR_CEREL | Q28235 cervus elap |
| 24 | 161.5 | 6.9 | 581 | LITR_MOUSE | P42702 mus musculu |
| 25 | 158 | 6.8 | 378 | IL3R_MOUSE | P26551 mus musculu |
| 26 | 157 | 6.8 | 896 | CYRB_MOUSE | P26955 mus musculu |
| 27 | 149 | 6.4 | 808 | IL3B_MOUSE | P26952 mus musculu |
| 28 | 146.5 | 6.3 | 608 | GHR_CHICK | Q02092 gallus gall |
| 29 | 145 | 6.2 | 634 | GHR_BOVIN | P79108 bos taurus |
| 30 | 145 | 6.2 | 638 | GHR_HUMAN | P10912 homo sapien |
| 31 | 144.5 | 6.2 | 1097 | LITR_HUMAN | P42702 homo sapien |
| 32 | 144 | 6.2 | 918 | IL3B_RAT | P40190 rattus norv |
| 33 | 142.5 | 6.1 | 917 | IL3B_MOUSE | Q00560 mus musculu |
| 34 | 141 | 6.1 | 611 | GHR_COLLI | Q90375 columba liv |
| 35 | 141 | 6.1 | 638 | GHR_PIG | P19756 sus scrofa |
| 36 | 140 | 6.0 | 638 | GHR_RABIT | P19941 oryctolagus |
| 37 | 139 | 6.0 | 508 | EPOR_HUMAN | P19235 homo sapien |
| 38 | 139 | 6.0 | 634 | GHR_SHEEP | Q28575 ovis aries |
| 39 | 135 | 5.8 | 638 | GHR_MACMU | P79194 macaca mula |

ALIGNMENTS:

| RESULT | 1 | STANDARD | PTI | 427 AA |
|------------|--|----------|-----|--------|
| IL31_HUMAN | | | | |
| AC | P78552: 099656: | | | |
| DT | 01-NOV-1997 (Rel. 35, Created) | | | |
| DT | 01-NOV-1997 (Rel. 35, Last sequence update) | | | |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update) | | | |
| DE | INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-13RA-1) | | | |
| GN | IL13RA1 OR IL13RA OR IL13R. | | | |
| CS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; | | | |
| CC | Eutheria; Primates; Catarrhini; Hominoidea; Homo. | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE-CARCINOMA; | | | |
| RX | MEDLINE: 97165986 | | | |
| RA | MILLOUX B., LAURENT P., BONNIN O., LUPKER J., CAPUT D., VITA N., FERRARA P., | | | |
| RT | "Cloning of the human IL-13R alpha1 chain and reconstitution with the IL1R alpha of a functional IL-4/IL-13 receptor complex." | | | |
| RL | FEBS Lett. 401:163-166(1997). | | | |
| RN | [12] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE-B-CELL; | | | |
| RA | GAUDHAT J.F.M., SCHLAGENHAUF E., FENG N.P., MOSER R., YAMAGI M., JEANIN P., ALOUANI S., ELSON G., NOTARANGELO L.D., WELLS T., | | | |
| RT | EUGSTER H.P., BONNEFOY J.Y.; | | | |
| RL | Submitted (Jan-1997) to the EMBL/Genbank/DBJ databases. | | | |
| RN | [13] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE-T-CELL; | | | |
| RX | MEDLINE: 97067184. | | | |
| RA | AMAN M.J., TAYEBI N., OBIRI N.I., PURI R.K., MODI W.S., | | | |
| RT | "CDNA cloning and characterization of the human Interleukin 13 receptor alpha chain." | | | |
| RL | J. Biol. Chem. 271:29265-29270(1996). | | | |
| CC | - FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY. | | | |
| CC | - SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA, IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS. | | | |
| CC | - TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS IN HEART, LIVER, SKELETAL MUSCLE AND OVARY; LOWEST LEVELS IN BRAIN, LUNG AND KIDNEY. ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS. | | | |
| CC | - SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN. | | | |
| CC | - SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN. | | | |
| CC | - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. | | | |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). | | | |
| CC | EMBL: Y10659; CAA71669.1; | | | |

40 134.5 5.8 557 1 INR1_HUMAN P17181 homo sapien
41 133.5 5.7 650 1 GHR_MOUSE P16882 mus musculu
42 130 5.6 560 1 INR1_BOVIN O04790 bos taurus
43 126.5 5.4 507 1 EPOR_RAT O07303 rattus norv
44 125.5 5.4 507 1 EPOR_MOUSE P14753 mus musculu
45 125 5.4 825 1 IL4R_HUMAN P24394 homo sapien

DR EMBL: Y09328; CAA70508.1; -
 DR EMBL: U62858; AAB37127.1; -
 DR HSSP: P31785; ILEN.
 DR MIM: 300119; -
 DR PFM: PF00041; fn3; 1.
 DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
 KW SIGNAL
 FT CHAIN 1 21 POTENTIAL.
 FT CHAIN 22 427 INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN.
 FT DOMAIN 22 343 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 344 367 POTENTIAL.
 FT DOMAIN 368 427 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 369 102 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 39 102 POTENTIAL.
 FT DISULFID 46 95 POTENTIAL.
 FT DISULFID 134 144 BY SIMILARITY.
 FT DISULFID 173 185 BY SIMILARITY.
 FT CARBOHYD 37 37 POTENTIAL.
 FT CARBOHYD 61 61 POTENTIAL.
 FT CARBOHYD 105 105 POTENTIAL.
 FT CARBOHYD 138 138 POTENTIAL.
 FT CARBOHYD 157 157 POTENTIAL.
 FT CARBOHYD 235 235 POTENTIAL.
 FT CARBOHYD 265 265 POTENTIAL.
 FT CARBOHYD 293 293 POTENTIAL.
 FT CARBOHYD 329 329 POTENTIAL.
 FT CARBOHYD 341 341 POTENTIAL.
 FT CARBOHYD 341 341 T -> I (IN REF. 3).
 FT CONFLICT 130 130 G -> D (IN REF. 3).
 FT CONFLICT 358 358
 FT SEQUENCE 427 AA: 48759 MM; 88533C57 CRC32;

Query Match 100.0%; Score 2324; DB 1; Length 427;
 Best Local Similarity 100.0%; Pred. No. 1,3-171;
 Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEMPARLGLMALLLCAGGGGGGGAAPETPTPTNLVSVENLCTIWTWNPPEGASS 60
 DB 1 MEMPARLGLMALLLCAGGGGGGGAAPETPTPTNLVSVENLCTIWTWNPPEGASS 60
 QY 61 NCSLWYFHFSGDKODKRIAPETRSIEVPLNERICLOVSGSCSTNESEKPSILVEKCI 120
 DB 61 NCSLWYFHFSGDKODKRIAPETRSIEVPLNERICLOVSGSCSTNESEKPSILVEKCI 120
 QY 121 PEGDESAVTELOCITWHLNLSYKCSWLPGRNTSPDNTLTLYWHSLEKIHOCENIFREG 180
 DB 121 PEGDESAVTELOCITWHLNLSYKCSWLPGRNTSPDNTLTLYWHSLEKIHOCENIFREG 180
 QY 181 QYFGSFDLTAKYKDSFEHSHVOIMKDNAGKIKPSFNIVPLTSRKPPPHIKNLSFHN 240
 DB 181 QYFGSFDLTAKYKDSFEHSHVOIMKDNAGKIKPSFNIVPLTSRKPPPHIKNLSFHN 240
 QY 241 DDLVQWENPQNFISRCLEYEVVNSQTEHNVFVQEAKECEPFEHREVENTSCFMP 300
 DB 241 DDLVQWENPQNFISRCLEYEVVNSQTEHNVFVQEAKECEPFEHREVENTSCFMP 300
 QY 301 GYLPTLNTVTRVNTKLCIEDDKLMSWSDMSIGKRNSTLYITMLIYVYAGAI 360
 DB 301 GYLPTLNTVTRVNTKLCIEDDKLMSWSDMSIGKRNSTLYITMLIYVYAGAI 360
 QY 361 IYLLYLKRLKIIIPPPDPGKIFKEMFGDONDTLHKKTDIYEKOKKEEDSVYLE 420
 DB 361 IYLLYLKRLKIIIPPPDPGKIFKEMFGDONDTLHKKTDIYEKOKKEEDSVYLE 420
 QY 421 NTKRASQ 427
 DB 421 NTKRASQ 427

RESULT 2
 ID 1131 MOUSE STANDARD; PRt: 424 AA.
 AC 009030;
 DT 01-NOV-1997 (Rel. 35, Created)
 *DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-13RA-1) (INTERLEUKIN-13 BINDING PROTEIN) (NR4).
 GN IL13RA1 OR IL13RA OR IL13R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC [1]
 RP SEQUENCE FROM N.A.
 RM MEDLINE: 96133964.
 RA HILTON D.J., ZHANG J.-G., METCALF D., ALEXANDER W.S., NICOLA N.A., WILSON T.A.,
 RT "Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).
 CC - FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY (BY SIMILARITY).
 CC - SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA, IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS (BY SIMILARITY).
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC - TISSUE SPECIFICITY: SPLEEN, LIVER, THYMUS, HEART, LUNG, KIDNEY, TESTIS, STOMACH, BRAIN, SKIN, AND COLON; BUT NOT SKELETAL MUSCLE.
 CC - SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC -
 DR EMBL: S80963; AAB50695.1; -
 DR MGD: MGI:105052; IL13RA.
 KM Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 424 INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN.
 FT DOMAIN 26 340 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 341 364 POTENTIAL.
 FT DOMAIN 365 424 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 367 100 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 44 93 POTENTIAL.
 FT DISULFID 132 142 BY SIMILARITY.
 FT DISULFID 171 183 BY SIMILARITY.
 FT CARBOHYD 35 35 POTENTIAL.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 103 103 POTENTIAL.
 FT CARBOHYD 136 136 POTENTIAL.
 FT CARBOHYD 262 262 POTENTIAL.
 FT CARBOHYD 338 338 POTENTIAL.
 FT SEQUENCE 424 AA: 48402 MM; 111E5963 CRC32;

Query Match 73.1%; Score 1698.5; DB 1; Length 424;
 Best Local Similarity 74.9%; Pred. No. 1,6-123;
 Matches 319; Conservative 40; Mismatches 64; Indels 3; Gaps 2;

QY 1 MEMPARLGLMALLLCAGGGGGGGAAPETPTPTNLVSVENLCTIWTWNPPEGASS 60
 DB 1 MEMPARLGLMALLLCAGGGGGGGAAPETPTPTNLVSVENLCTIWTWNPPEGASS 60
 QY 61 NCSLWYFHFSGDKODKRIAPETRSIEVPLNERICLOVSGSCSTNESEKPSILVEKCI 120
 DB 61 NCSLWYFHFSGDKODKRIAPETRSIEVPLNERICLOVSGSCSTNESEKPSILVEKCI 120
 QY 121 PEGDESAVTELOCITWHLNLSYKCSWLPGRNTSPDNTLTLYWHSLEKIHOCENIFREG 180
 DB 121 PEGDESAVTELOCITWHLNLSYKCSWLPGRNTSPDNTLTLYWHSLEKIHOCENIFREG 180
 QY 181 QYFGSFDLTAKYKDSFEHSHVOIMKDNAGKIKPSFNIVPLTSRKPPPHIKNLSFHN 240
 DB 181 QYFGSFDLTAKYKDSFEHSHVOIMKDNAGKIKPSFNIVPLTSRKPPPHIKNLSFHN 240
 QY 241 DDLVQWENPQNFISRCLEYEVVNSQTEHNVFVQEAKECEPFEHREVENTSCFMP 300
 DB 241 DDLVQWENPQNFISRCLEYEVVNSQTEHNVFVQEAKECEPFEHREVENTSCFMP 300
 QY 301 GYLPTLNTVTRVNTKLCIEDDKLMSWSDMSIGKRNSTLYITMLIYVYAGAI 360
 DB 301 GYLPTLNTVTRVNTKLCIEDDKLMSWSDMSIGKRNSTLYITMLIYVYAGAI 360
 QY 361 IYLLYLKRLKIIIPPPDPGKIFKEMFGDONDTLHKKTDIYEKOKKEEDSVYLE 420
 DB 361 IYLLYLKRLKIIIPPPDPGKIFKEMFGDONDTLHKKTDIYEKOKKEEDSVYLE 420
 QY 421 NTKRASQ 427
 DB 421 NTKRASQ 427

Query Match 13.7%, Score 318; DB 1; Length 415;
Best Local Similarity: 23.9%, Pred. No. 2,46-17;
Matches 97; Conservative 74; Mismatches 119; Indels 56; Gaps 14;

| | | | |
|----|-----|--|-----|
| QY | 33 | PPVNLVSVENLCVITWNP-PEGASSNCSLWTFSHF-GDKQDKLAPETRRSIEVPL | 90 |
| DB | 29 | PPV-NEFTIKAGLAAVLLHMDPNPQEOHRHDLXHVAINAPQEDIEDYTRKTESKCVPL | 87 |
| QY | 91 | NERILGCGSCSTSESKPSILVFKKCSIPRGDESAVTELOCIMHNL----- | 140 |
| DB | 88 | HEGFAASFTLIKSSHTLLASSWSAEIKAPGSGSTVNLCTTHVYSSHTLRPYQ | 147 |
| QY | 140 | SYMCSSAPGRNTSPDNYTLTYWHRSLXIHOCENIRE-GGYFGCSFDLTAKYDSF | 197 |
| DB | 148 | VSRLCTETLVGDAPEDTQYFLYRGVLTLE-KQGEYRDALNRTACMPRTFINSKGF | 205 |
| QY | 198 | EQHSQIVLYKDNAGIKRSEFNVLPTSRYKDPDPPIKULSFHNDLIYQWENPQN-FLSR | 256 |
| DB | 206 | EQLAHVINGSSKRAIKKPFQDLFSLADQVNPNNVVEIESNLSYIQWENPLSAFPDH | 265 |
| QY | 257 | CLVEVEVNNQSOTETHANFEYQEAECENPEFEERNVENTSCFVNPGLDPLTVLRVKT | 316 |
| DB | 266 | CENVELKIYNNKNG-----HIQEKLIANKPLSKIDDVY-----SIVRAAV | 309 |
| QY | 317 | NKLYEDDKLMSNMSQENSIGKRRNSTLYITMLLIVPIVAGAILVLLYKRLKI--- | 374 |
| DB | 310 | SSPCMPGR-GEWNSQPIYVGKERKS-LVEMHLIYLP--TAACEVLLIFSLICVCHLM | 364 |
| QY | 374 | -IIFPIPDGKIFKEWEGDNDLHMKKADYIEKQKEEDSVY | 417 |
| DB | 365 | TRLEFPVPAPKSNFKDL-----PVVTEIEKPSNEKIEVY | 399 |

RESULT 4
IL5R HUMAN
ID IL5R HUMAN STANDARD; PRT: 420 AA.
AC Q01344;
DT 01-JUL-1993 (Rel. 26, Created)
DE 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA) (CD125 ANTIGEN).
GZ IL5RA OR IL5R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP MEDLINE: 52372031.
RA SCOTT H.S., GUO X.H., HOPWOOD J.J., MORRIS C.P.;
RT "Structure and sequence of the human alpha-L-iduronidase gene";
RL Genomics 13:1311-1313(1992).
RN [2]
RP MEDLINE: 9235767.
RA TAVERNIER J., TUYPPENS T., PLAETINCK G., VERHEE A., PIERS W.,
RT "Molecular basis of the membrane-anchored and two soluble isoforms of the human interleukin 5 receptor alpha subunit";
RL Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
RN [3]
RP MEDLINE: 92935669.
RA TAVERNIER J., DEVOS R., CORNELIS S., TUYPPENS T., VAN DER HEYDEN J.,
RT "A human high affinity interleukin-5 receptor (IL5R) is composed of

```

RT an IL5-specific alpha chain and a beta chain shared with the receptor
RT for GM-CSF.
RL Cell 66:1175-1184(1991).
CC -1- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC BINDS TO IL-5.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: THREE ISOFORMS, TWO SOLUBLE FORMS AND A
CC MEMBRANE-BOUND FORM EXIST DUE TO ALTERNATIVE SPLICING OF THE
CC SAME GENE.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -1- DATABASE: NAME-PROW; NOTE-CD guide Cdw125 entry;
CC WWW-http://www.ncbi.nlm.nih.gov/prov/cd/cdw125.htm.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M96652; AAA59152.1; -
CC EMBL; M96651; AAA59151.1; -
CC EMBL; M75914; AAA36110.1; -
CC EMBL; A26249; CAA01793.1; -
CC EMBL; A24587; CAA01731.1; -
CC EMBL; A26251; CAA01794.1; -
CC PIR; A40267; A40267.
CC DR MIM; 147851; -
CC DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; FALSE_NEG.
CC DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
CC KM Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
CC FT CHAIN 1 420 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
CC FT DOMAIN 21 342 EXTRACELLULAR (POTENTIAL).
CC FT TRANSSEM 343 362 POTENTIAL.
CC FT DOMAIN 363 420 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 35 35 POTENTIAL.
CC FT CARBOHYD 131 131 POTENTIAL.
CC FT CARBOHYD 216 216 POTENTIAL.
CC FT CARBOHYD 244 244 POTENTIAL.
CC FT VARSPIC 333 335 NDE -> FSR (IN SOLUBLE ISOFORM S1).
CC FT VARSPIC 336 420 MISSING (IN SOLUBLE ISOFORM S1).
CC FT VARSPIC 333 333 N -> K (IN SOLUBLE ISOFORM S2).
CC FT VARSPIC 334 420 MISSING (IN SOLUBLE ISOFORM S2).
CC FT VARSPIC 334 420 MISSING (IN SOLUBLE ISOFORM S2).
CC SQ SEQUENCE 420 AA; 47700 MW; 75C19847 CRC32;

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Query Match 12.88; Score 296.5; DB 1; Length 420;
Best Local Similarity 24.88; Pred. No. 1.1e-15;
Matches 102; Conservative 65; Mismatches 180; Indels 65; Gaps 16;

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QY 33 PPTVNLVSVENLTCTVMTWNP-PEGASSNCSLWYFHFQDKQDKIAPETRRSIEVPLN 91
DB 32 PPTVNLVSVENLTCTVMTWNP-PEGASSNCSLWYFHFQDKQDKIAPETRRSIEVPLN 91
QY 92 ERICLOV-----GSCSTNESEKPSILVEKCS-----PPSDPSAVTELOCITVHNL--- 140
DB 83 ESKCVTLHKGFSAVFTIIONDSILASSWASSELNAPSPGTSIYVNLCTTNTEDN 142
QY 140 -----SY-----MKSGMLGRNTSPNTLYLYWHSLEKIHCCENIFRE--GQYGGCSPDL 189
DB 143 YSRKRSQVSIHCHTWLGTDPEDTOYFLYIRYSWTE--ECQYSDTLGRNIAQWPPR 200
QY 190 TKVDSSEFQHSVOIMKDNAGIKRPSINIVPLTSRYKPDPPHKNLSFHNDDLYVOMEN 249
DB 201 TFLSKGRDMLSVLVNSSKSAIRPFQDLALAIQINPLVNTVAIESTRISIQMEK 260
QY 250 PGN-FISRCLEFVEVNNSTQETINNVFVOEAKENPFEERNVENTSCFVGLPDTLN 308

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DB 261 PVSAFPHCHDEYKIKHNTENG-----YLQIEKMTNNAFISIDLSKY----- 305
QY 309 TVAPRTVNTKCYEDDKLMSNMOESIGKRKSTLYITMLVPIVGAIVLLLYLK 368
DB 305 DVQVRAVSSMCREDAG-LNSENSOPIVGNDEKPLREMFVIMATTCILILSLICK 363
QY 369 --RLKIIIFPPDPGKIFEMFGDONDDTLHWKKYDIYEKQTKRETSVYL 418
DB 364 ICHMIKIFPPDPAPSPNIMDLVTIN-----YKASSSEIEIVI 404

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RESULT 5

| ID | 1132_HUMAN | STANDARD; | PRT; | 380 AA. |
|----|---|-----------|------|---------|
| AC | 014627; | 000667; | | |
| DT | 01-NOV-1997 (Rel. 35, Created) | | | |
| DT | 01-NOV-1997 (Rel. 35, Last sequence update) | | | |
| DE | 15-JUL-1999 (Rel. 38, Last annotation update) | | | |
| DE | INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR (INTERLEUKIN-13 BINDING PROTEIN). | | | |
| GN | IL13RA2 OR IL13R. | | | |
| OS | Homo sapiens (human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; | | | |
| OC | Eutheria; Primates; Catarrhini; Hominoidea; Homo. | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=RENAL CELL CARCINOMA; | | | |
| RX | MEDLINE, 96279273 | | | |
| RA | CAPUT D., LAURENT P., KAGHAD M., LELINS J.M., LEFORT S., VITA N., | | | |
| RA | TERRANA P., | | | |
| RT | Cloning and characterization of a specific interleukin (IL)-13 | | | |
| RT | binding protein structurally related to the IL-5 receptor alpha | | | |
| RT | chain. | | | |
| RL | J. Biol. Chem. 271:16921-16926(1996). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=TESTIS; | | | |
| RA | DONALDSON D.D., WHITTERS M.J., FITZ L., NEBEN T., FINNERTY H., | | | |
| RA | HENDERSON S.L., O'HARA R.M. JR., TURNER K.J., WOOD C.R., COLLINS M., | | | |
| RL | Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases. | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=BRAIN; | | | |
| RA | GUO J., MINVILLE S., | | | |
| RL | Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases. | | | |
| CC | -1- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13 | | | |
| CC | (IL-13), BUT NOT TO IL-4. | | | |
| CC | -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. | | | |
| CC | -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN. | | | |
| CC | -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. | | | |
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| CC | entities requires a license agreement (See http://www.isb-sib.ch/announce/ | | | |
| CC | or send an email to license@isb-sib.ch). | | | |
| CC | EMBL; X95302; CAA64617.1; - | | | |
| CC | EMBL; U70981; AAB17170.1; - | | | |
| CC | EMBL; Y08768; CAA70021.1; - | | | |
| CC | MIM; 300130; - | | | |
| CC | PRIM; PF00041; fn3; 1. | | | |
| CC | PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1. | | | |
| CC | Receptor; Transmembrane; Glycoprotein; Signal. | | | |
| CC | FT CHAIN 1 380 POTENTIAL. | | | |
| CC | FT CHAIN 27 380 INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN. | | | |
| CC | FT DOMAIN 27 343 EXTRACELLULAR (POTENTIAL). | | | |
| CC | FT TRANSSEM 344 363 POTENTIAL. | | | |
| CC | FT DOMAIN 364 380 CYTOPLASMIC (POTENTIAL). | | | |
| CC | FT DISULFID 145 155 BY SIMILARITY. | | | |

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 9.8% | Score 228; | DB 1; | Length 400; |
| Best Local Similarity | 22.4% | Pred. No. 1.9e-10; | | |
| Matches 90; | Conservative 82; | Mismatches 180; | Indels 50; | Gaps 18; |

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QY 31 TOPPVNLSVSNENCTVYIWTNNPPEGAS-SUCSJMFTSFHEDKODKKAETRISIEVP 89
Db 29 TVAPASSLLWREDSR-TMNLSDWCCEINTFSKCFJ-----TDKKNRVVEPRLSNNECSC 81
QY 90 LNERICLOYGOSOCSTNESEKPSILVEKCSISPEGPDRESATVETLQCIWNHLSYMCMSLPG 149
Db 82 TFEICLHGVTAEVYHAVNVSQKGFQOKLLYPHSGHEGTAQNFSCFTYIMADLMNCTWARG 141
QY 150 RMTSPDINTLLYIMHRSLEKIHOCNIFRE-GQYFGCSFD-LTKYKDSFEQHSVQJLMVK 207
Db 142 PTAHPRVOYFYLIRNSKRREIRCEPYIJDOSGTHVGHCHLMLSGLLSNRY-----PLVN 195
QY 208 DNAGKIKRPSF--NIYPLTSRVKPDPEPHIKNLSFHDDLYOMENPQNF--ISRCLF-YEV 262
Db 196 GTSREIGLOFPELSLDTKIERFNPSPNVATRCMTHCLVWKQPRYOKSLYDEQYOL 255
QY 265 EYN--NSQTEHNHFVYOACACENPEEFERNVENTSCFVPCVLPDLNTVYIRIKTKKLC 320
Db 256 DVHRRKTOPTGENTLLINVSGLERN-----YNPSEPRAHASHVAKIRADVRIL 304
QY 321 YEDKLLMNMSQEMSIGKRRKS--TLTYMLLIYVYAGAIYVLLLYLKLRI-IIIFP 377
Db 305 N-----WMSWEALIEFGDDGNDGSLKSYIYVLLIYGLTYVCG-YVLGFKRFNRLQIÖRLEFP 358
QY 378 IPDBEKIFKEFEGDQÑ--DPTLHKRKYDIYE-KQTKRETSYD 416
Db 359 VPQ-----IKOKLNDNHVEEDITMEETPEBGKGKYREEVLTU 396

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RESULT 7
CYRG CANFA
ID CYRG CANFA STANDARD: PRT: 373 AA.
AC P40321.
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
OS IL2RG
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPLEEN.
RX MEDLINE: 95130114.
RA HEMTHORN P.S., SOMBERG R.L., FIMMANT V.M., PUCK J.M., PATERSON D.F.,
RA FELSBRG P.J.;
RT "IL-2R gamma gene microdeletion demonstrates that canine X-linked
RT severe combined immunodeficiency is a homologue of the human
RT disease".
RT Genomics 23:69-74(1994).
RL -1 INTERLEUKIN.
RL -1 FUNCTION. COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -1 SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1 DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED
CC SEVERE COMBINED IMMUNODEFICIENCY.
CC -1 SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1 SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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| | | | |
|----------|--|-----|-----|
| DR | EMBL: U04361; AAC48403.1; - | | |
| LR | HSSP: P31785; ILIN. | | |
| DR | PEAM: PF00041; fn3. 1. | | |
| DR | PROSITE: PS00341; RECEPTOR_CYTOKINES_1; 1. | | |
| DR | PROSITE: PS00340; RECEPTOR_CYTOKINES_2; FALSE_NEG. | | |
| KM | Receptor; Transmembrane; Glycoprotein; signal. | | |
| ET | SIGNAL | 1 | 22 |
| ET | CHAIN | 23 | 373 |
| ET | DOMAIN | 23 | 261 |
| ET | TRANSMEM | 262 | 283 |
| ET | DOMAIN | 284 | 373 |
| ET | DOMAIN | 151 | 249 |
| ET | DISULFID | 62 | 72 |
| ET | DISULFID | 102 | 115 |
| ET | CARBOHYD | 24 | 24 |
| ET | CARBOHYD | 71 | 71 |
| ET | CARBOHYD | 75 | 75 |
| ET | CARBOHYD | 84 | 84 |
| ET | CARBOHYD | 159 | 159 |
| ET | CARBOHYD | 164 | 164 |
| ET | CARBOHYD | 249 | 249 |
| SEQUENCE | 373 AA; 42516 MW; 6FD017ED CXC32; | | |

| | | | | |
|------------------------|------------------|--------------------|------------|-------------|
| Query Match: | 8.98; | Score 207; | DB 1; | Length 373; |
| Best Local Similarity: | 25.18; | Pred. No. 7.3e-09; | | |
| Matches 76; | Conservative 52; | Mismatches 131; | Indels 44; | Gaps 14; |

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QY 88 VPLNERICLQVQSCSTNSKSPSLIVEKCIIPPEGDEASATELOCITWHLNLSYKCSML 14
Dh 21 VGNSTVPMNG-----NEDITPDEFIATPBEITLSVSLPLPEVQCVFWEYINCTWN 75
QY 148 PGNTPSDPNNITLYYHRSL--EKIHOCEN-IFRGQYFGCSFDLTTRYKSSFEQHSVOI 204
Dh 76 SSSEPPR-TNLTLLHWYKNSNDCKQEGCHLFSREYTAGCW--LQKEEHLIETFYVL 132
QY 205 MYVNDAGKIKPSPENIYPLTSRYKPPRPKILNSFN--DDLQWQENPQWFIKRCIYE 266
Dh 133 --RDPREPRQSTQKTKLQNLVTPAP--ENITLHNLSQSELEISWSN--RHIDHCLEHV 186
QY 362 VEVNNSQITHAVFYVOAKCENPEFEENVENTSCFMYPGVLPDTLNTVIRYKTKCY 321
Dh 187 VQYRSQWDSKT-----EQSDVHRNSFSLPSVDQKFTFVRNRSYNPLCG 232
QY 322 EDDKLSMNSQCSMISGK--KRNSTLYIMLLIVYVYAGAIYVL--LYLKRKIITFP 376
Dh 233 SNAQ-WSEMSHPIHNGSNTSKENPLFSEAVLPLGSMGLIISLICYWTLER----SIP 287
QY 377 PTP 379
Dh 288 RIP 290

RESULT 8
CYRG_MOUSE
IT1 CYRG_MOUSE STANDARD; 4 PRT; 369 AA.
AC. P34902;
Df 01-FEB-1994 (Rel. 28, Created)
Df 01-FEB-1994 (Rel. 28, Last sequence update)
Df 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
Os Mus musculus.(Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Rf [1]
Rp SEQUENCE FROM N.A.
RX MEDLINE; 33277575.
VA KIMAKI S., KONDO M., TAKESHITA T., ASAO H., NAKAMURA M., SUGAMURA K.

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NW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT CHAIN 23 369 BY SIMILARITY.
FT DOMAIN 23 263 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT TRANSMEM 264 284 POTENTIAL.
FT DOMAIN 285 369 CYTOPLASMIC (POTENTIAL).
FT DISULFID 62 72 FIBRONECTIN TYPE-III.
FT DISULFID 102 115 POTENTIAL.
FT CARBOHYD 71 71 POTENTIAL.
FT CARBOHYD 75 75 POTENTIAL.
FT CARBOHYD 84 84 POTENTIAL.
FT CARBOHYD 96 96 POTENTIAL.
FT CARBOHYD 159 159 POTENTIAL.
FT CARBOHYD 164 164 POTENTIAL.
FT SEQUENCE 369 AA; 42241 MW; 60230827 CRC32;

Query Match 8.8%; Score 205.5; DB 1; Length 369;
Best Local Similarity 24.0%; Pred. No. 9.4e-09;
Matches 76; Conservative 63; Mismatches 121; Indels 57; Gaps 16;

C7 103 STFSSEKPSILVKEKISPPEDGPEANVLEQICIMNLSYMKCSMLPGRTSPD---TNT 159
C6 31 SANEDIKADLIITSTAPEHLSAPTLPLEVQCEVENIEEMNTW---NSSESPATNT 86
C5 160 LYYHRSLEKIHOCENIFREGOFCGSEDLTVKXKSEFQHSVQ-----INVKDNAGKI 213
C4 87 LHYRKYVD-----NNTQECHELYFSNEIT--SSCQIQKEDIQLYQTFVQLODPQRKQ 139
C3 214 KPSFIVPLTSVNPDPPIHKNLSFH--DDLYQWENPQNFISCLFEYEVNNSQTE 270
C2 140 RLYVAKMLQNIYIRAP--ENLITLSNSESQLEDRKMS-RIKIKERCLQYLVQYRSNDR 196
C1 271 TNHNVYQEAKEENPEFRNVENTSCFVMPGVGLPPTLN--TVIRVTKTKLCEDDKLS 328
D6 197 SFT-----ELIVNHERFSIPSV--DEKRYTRVRSRNPICGSSQQ-WS 239
C7 329 NWSQMSIGK---KRNSTLYITMLDIVYVAGAVITLL--YKRLKIIFPIPDG 382
D6 246 KMSQVHMVSHVEENPSIFALEAVLIPVGTGLITLIFYVCMLERM-----PIIP-PI 293
C7 383 KIKFEMGDQNDLTLHW 399
D6 294 KNEDELVTEYQGNFSAW 310

RESULT 9
CYRG_HUMAN STANDARD: PRT; 369 AA.
ID CYRG_HUMAN 231785;
D1 01-JUL-1993 (Rel. 26, Created)
D2 01-JUL-1993 (Rel. 26, Last sequence update)
D3 15-DEC-1998 (Rel. 37, Last annotation update)
D4 CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C) (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64) (CD132 ANTIGEN).
D5 IL2RG.
D6 Homo sapiens (Human).
D7 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
D8 Eutheria; Primates; Catarrhini; Homiidae; Homo.
D9 [1]
D10 SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
D11 MEDLINE: 92335883.
D12 TAKEISHITA T., ASAO H., OHTANI K., ISHII N., KUMAKI S., TANAKA N.,
D13 MUKAKATA H., NAKAMURA M., SUGAWARA K.;
D14 "Cloning of the gamma chain of the human IL-2 receptor.";
D15 Science 257:379-382(1992).
D16 [3]
D17 SEQUENCE FROM N.A.
D18 TISSUE-LIVER.
D19 MEDLINE: 93293887.
D20 NOUCHI M., ADESTEIN S., CAO X., LEONARD W.J.;
D21 "Characterization of the human interleukin-2 receptor gamma chain
```

RT gene".
 RL J. Biol. Chem. 268:13601-13608(1993).
 [3]
 RP SEQUENCE FROM N.A., AND VARIANTS ASP-114 AND ASN-153.
 RX MEDLINE: 94004847.
 RA PUCK J.M., DESCHERES S.M., PORTER J.C., DOTRA A.S., BROWN C.J.,
 RA WILLARD H., HENTHORN P.S.;
 RT "The interleukin-2 receptor gamma chain maps to xq13.1 and is mutated
 in X-linked severe combined immunodeficiency. SCID1.";
 RL Hum. Mol. Genet. 2:1099-1104(1993).
 [4]
 RP IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE: 94090315.
 RA KONDO M., TAKESHITA T., ISHII N., NAKAMURA M., WATANABE S.,
 RA ARAI K.-I., SUGAMURA K.;
 RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between
 receptors for IL-2 and IL-4.";
 RL Science 262:1874-1877(1993).
 [5]
 RP IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE: 94090317.
 RA RUSSELL S.M., KEGAN A.D., HARADA N., NAKAMURA Y., NOGUCHI M.,
 RA LELAND P., FRIEDMAN M.C., MIYAJIMA A., PURI R.K., PAUL W.E.,
 RA LEONARD W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 interleukin-4 receptor.";
 RL Science 262:1880-1883(1993).
 [6]
 RP IDENTIFICATION AS A IL-7R SUBUNIT.
 RX MEDLINE: 94090316.
 RA NOGUCHI M., NAKAMURA Y., RUSSELL S.M., ZIEGLER S.F., TSANG M., CHAO X.,
 RA LEONARD W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 interleukin-7 receptor.";
 RL Science 262:1877-1880(1993).
 [7]
 RP 3D-STRUCTURE MODELING OF 57-248.
 RX MEDLINE: 95111955.
 RA BAMBOURGH P., HEDGECOCK C.J., RICHARDS W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 modelling.";
 RL Structure 2:839-851(1994).
 [8]
 RP VARIANTS XSCID PHE-115; CYS-240 AND ILE-241.
 RX MEDLINE: 94130970.
 RA DISANTO J.P., DAUTRY-VARSAT A., CERTAIN S., FISCHER A.,
 RA DE SAINT BASILE G.;
 RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked
 severe combined immunodeficiency disease result in the loss of
 high-affinity IL-2 receptor binding.";
 RL Eur. J. Immunol. 24:475-479(1994).
 [9]
 RP VARIANT XSCID LYS-68.
 RX MEDLINE: 94375038.
 RA MARLEWICZ S., SUBTIL A., DAUTRY-VARSAT A., FISCHER A.,
 RA DE SAINT BASILE G.;
 RT "Detection of three nonsense mutations and one missense mutation in
 the interleukin-2 receptor gamma chain gene in SCID1 that
 differentially affect the mRNA processing.";
 RL Genomics 21:291-293(1994).
 [10]
 RP VARIANT XSCID HIS-162.
 RX MEDLINE: 94300093.
 RA ISHII N., ASAO H., KIMURA Y., TAKESHITA T., NAKAMURA M., TSUCHIYA S.,
 RA KONNO T., MAEDA M., UCHIYAMA T., SUGAMURA K.;
 RT "Impairment of ligand binding and growth signaling of mutant IL-2
 receptor gamma-chains in patients with X-linked severe combined
 immunodeficiency.";
 RL J. Immunol. 153:1310-1317(1994).
 [11]
 RP VARIANT XSCID ASN-39.
 RX MEDLINE: 95023932.
 RA DISANTO J.P., RIEUX-LAUCAT F., DAUTRY-VARSAT A., FISCHER A.,
 RA DE SAINT BASILE G.;
 RT "Defective human interleukin 2 receptor gamma chain in an atypical X
 chromosome-linked severe combined immunodeficiency with peripheral T
 cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470(1994).
 [12]
 RP VARIANTS XSCID CYS-226 AND HIS-226.
 RX MEDLINE: 95397841.
 RA PEPPER A.E., BUCKLEY R.H., SMALL T.N., PUCK J.M.;
 RT "Two mutational hotspots in the interleukin-2 receptor gamma chain
 gene causing human X-linked severe combined immunodeficiency.";
 RL Am. J. Hum. Genet. 57:564-571(1995).
 [13]
 RP VARIANT XSCID SER-183.
 RX MEDLINE: 96013903.
 RA CLARK P.A., LESTER T., GENET S., JONES A.M., HENDRIKS R.,
 RA LEVINSKY R.L., KINNON C.;
 RT "Screening for mutations causing X-linked severe combined
 immunodeficiency in the IL-2R gamma chain gene by single-strand
 conformation polymorphism analysis.";
 RL Hum. Genet. 96:427-432(1995).
 [14]
 RP VARIANT XSCID GLN-TRP INS-237.
 RX MEDLINE: 95164726.
 RA PUCK J.M., PEPPER A.E., BEDARD P.-M., LAFRANCOISE R.;
 RT "Female germ line mosaicism as the origin of a unique IL-2 receptor
 gamma-chain mutation causing X-linked severe combined
 immunodeficiency.";
 RL J. Clin. Invest. 95:895-899(1995).
 [15]
 RP VARIANT XSCID GLN-271.
 RX MEDLINE: 95190013.
 RA SCHWALSTIEG F.C., LEONARD W.J., NOGUCHI M., BERG M., RUDLOFF H.E.,
 RA DENNEY R.M., DAVE S.K., BROOKS E.G., GOLDMAN A.S.;
 RT "Missense mutation in exon 7 of the common gamma chain gene causes a
 moderate form of X-linked combined immunodeficiency.";
 RL J. Clin. Invest. 95:1169-1173(1995).
 [16]
 RP VARIANT XSCID ARG-115.
 RX MEDLINE: 97042245.
 RA STEPHAN V., WAHN V., LE DEIST F., DIRKSEN U., BROKER B.,
 RA MULLER-FLECKENSTEIN I., HORNFEFF G., SCHOTEN H., FISCHER A.,
 RA DE SAINT BASILE G.;
 RT "Atypical X-linked severe combined immunodeficiency due to possible
 spontaneous reversion of the genetic defect in T cells.";
 RL New Engl. J. Med. 335:1563-1567(1996).
 [17]
 RP VARIANT XSCID GLN-285.
 RX MEDLINE: 97295088.
 RA JONES A.M., CLARK P.A., KATZ F., GENET S., MCMAHON C., ALTERMAN L.,
 RA CANT A., KINNON C.;
 RT "B-cell-negative severe combined immunodeficiency associated with a
 common gamma chain mutation.";
 RL Hum. Genet. 99:677-680(1997).
 [18]
 RP VARIANT XSCID CYS-222.
 RX MEDLINE: 98064061.
 RA SHARFE N., SHAHAR M., ROIFMAN C.M.;
 RT "An interleukin-2 receptor gamma chain mutation with normal thymus
 morphology.";
 RL J. Clin. Invest. 100:3036-3043(1997).
 [19]
 RP FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 INTERLEUKINS.
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 IL-13 RECEPTORS.
 CC -1- PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED
 IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMMAGLOBULINEMIA, SWISS TYPE
 OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD132 entry;
 WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd132.htm".

CC -1- DATABASE: NAME=IL2RChase; NOTE=x-linked SCID mutation database;
 CC WWW="http://www.hbgrl.nih.gov/DIR/LGT/SCID/IL2RChase.html".
 CC
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 CC
 CC EMBL: D11086; BAA01857.1; -
 CC EMBL: L12183; AAA59145.1; -
 CC EMBL: L12178; AAA59145.1; JOINED.
 CC EMBL: L12176; AAA59145.1; JOINED.
 CC EMBL: L12177; AAA59145.1; JOINED.
 CC EMBL: L12179; AAA59145.1; JOINED.
 CC EMBL: L12180; AAA59145.1; JOINED.
 CC EMBL: L12181; AAA59145.1; JOINED.
 CC EMBL: L12182; AAA59145.1; JOINED.
 CC EMBL: L19546; AAC37524.1; -
 CC PIR: A42565; A42565.
 CC PDB: 1ILM; 26-JAN-95.
 CC PDB: 1ILN; 26-JAN-95.
 CC MIM: 300400; -
 CC MIM: 308380; -
 CC PRAM: PR00041; fn3; 1
 CC PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 CC PROSITE: PS00340; RECEPTOR_CYTOKINES_2; FALSE_NEG.
 CC DR PROSITE: Transmembrane; Glycoprotein; Signal; Disease mutation;
 CC Receptor;
 KW
 Query Match 8.7%; Score 202; DB 1; Length 369;
 Best Local Similarity 27.2%; Pred. No. 1,7e-08;
 Matches 72; Conservative 44; Mismatches 101; Indels 48; Gaps 14;
 QY 131 ELQCIWHNLSYMKCSWLPGRNTSPDNTYLYWHRSL-EKIHOCEN-IFREGYFGCSF 187
 DB 59 EVGCEFFVNEVWNCMTNMSSEPPQ-TKLTLYWYKNSDNDKVKCHYLPSSEITSGC- 116
 QY 188 DLFKVDSSFEQHSVOQIMVNDNAGKIKPSFNIVPLTSRVAPDPDPHINKLSF--NDLY 244
 DB 116 QLOKKEHLVQTFVYOL--ODPREPRROATQMLQNLVLPWPV--ENLTLHLKLSOLE 171
 QY 245 VOMENPQNFISRLT---FYEVEVNNSTQETHNHFYQEAKECEPERVENNTSCFMP 300
 DB 172 LNNNN--RFLNHCLEHLVQTRTMDISWT-----EQSDVRHKSFLP 211
 QY 301 GVLPTDLNIVIRIKTKLCEYEDDKLMSNMSOEMSIG--KRNSTLYITMLLIVPIVA 357
 DB 212 SVGQKRYTRFVRSRFPPLC-GSAQHSWSESHPIHMGSTNSKEPFLFALEAVISVGS 270
 QY 358 GAIIVLL--LYLKRKLITPPPI 379
 DB 271 GLIISLCVYFWLER---TMPRIIP 291
 RESULT 10
 ID PRUR_MELGA STANDARD; PRT; 831 AA.
 AC 091094; 091091; 091092;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (TPRLR).
 GN PRLR.
 OS Meleagris gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Archosauria; Aves;
 OC Neognathae; Galliformes; Meleagrididae; Meleagris.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RC MEDLINE: 97057891.
 RA ZHOU J.F., ZADWORYN D., GUERENE D., KUHNLEIN U.;

RT "Molecular cloning, tissue distribution, and expression of the
 RT prolactin receptor during various reproductive states in Meleagris
 RT gallopavo".
 RU Biol. Reprod. 55:1081-1090(1996).
 RN [2]
 RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
 RC TISSUE-Ovary;
 RA PWTSG R., YOG S.K., FOSTER D.N., EL HALAMANI N.E.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DDA databases.
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC
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 CC
 CC EMBL: L76587; AAB01544.1; -
 CC EMBL: U22947; AAA75038.1; -
 CC EMBL: U22924; AAA75039.1; -
 CC HSSP: P16471; 1BP3.
 CC PRAM: PR00041; fn3; 4
 CC PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 2.
 CC PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 2.
 CC DR PROSITE: Transmembrane; Glycoprotein; Signal; Repeat.
 KW
 Query Match 8.5%; Score 198.5; DB 1; Length 831;
 Best Local Similarity 23.3%; Pred. No. 9.3e-08;
 Matches 92; Conservative 59; Mismatches 157; Indels 87; Gaps 20;
 QY 33 QP--PVTNLSVVENLCTV--IWT-WNPP--EGASSNCSLWYFSGDKODKRIAPETR 84
 DB 126 QPSPV-NLTLETQRYANIMYLAKKMSPPLADASSN---HHYH---ELRUKPEKE 176
 QY 85 SIE-VPLNERICQVQSCSTNE-----SEKSLIVKCIISP 120
 DB 177 EWEIVPG-----VQIOCKINRLNAGMRYVQRCMLDGESEMSSEERRILISGLSP 230
 QY 121 PEDPSAVTELOCIWHNLSYMKCSWLPGRNTSPDNTYLYWHRSL-EKIHOCENIFREG 180
 DB 231 PE-----KPIITKCRSEKFTFCWKKPGLDGHPIYNTILLYSKBEEOVYECPP-YRTA 284
 QY 181 QYFGCSFDLTKVVDSSFEQHSVOIMVNDNAGKIKPSFNIVPLTSRVKPPDP-----HIKN 235
 DB 285 GPSICVFD--KKHISFWYVYNTVKAATNEMGSNSDPHYVDYVYIYQDPDPANVTLELTK 342

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CC EMBL: U33748; AAB07812.1;
 DR HSSP; P31785; 11LN.
 DR PFAM; PF00041; fn3; 1.
 DR PROSITE; PS00241; RECEPTOR-CYTOKINES_1; 1.
 DR PROSITE; PS00340; RECEPTOR-CYTOKINES_2; FALSE NEG.
 DR Receptor; Transmembrane; Glycoprotein; signal.
 FT SIGNAL 1 22
 FT CHAIN 23 379
 FT DOMAIN 23 269
 FT TRANSMEM 270 290
 FT DOMAIN 291 379
 FT DOMAIN 158 256
 FT DISULFID 168 78
 FT DISULFID 109 122
 FT CARBOHYD 77 77
 FT CARBOHYD 81 81
 FT CARBOHYD 90 90
 FT CARBOHYD 166 166
 FT CARBOHYD 171 171
 FT CARBOHYD 171 171
 FT SEQUENCE 379 AA; 43037 MW; 52EF5D72 CRC32;

Query Match 8.5%; Score 197; DB 1; Length 379;

Best Local Similarity 23.8%; Pred. No. 4,4e-08; Mismatches 110; Indels 46; Gaps 13;

Matches 67; Conservative 58; Mismatches 110; Indels 46; Gaps 13;
 QY 119 SPREGPESA---VTELOCIWHLNLSYKCSMLPGRNTSPDNTLYWHSRL---EKIHQ 172
 DB 50 STAGTLDVSTLPLPKYQCEVFNEYMNCTWNSSEPOPN-NLTHYGHNFNDDKLOE 108
 QY 173 CEN-IRREGGYPCSPFLTVKXSSFEQHSVOIM-VKDNAGKIKRSPNIYPLTSRVAPDP 230
 DB 109 CGHYLSEGITSCWFGKKEIR--LYETFYVQLODPRHKKOPOMKLDLDTVPAPEN 166
 QY 231 PHAKNLSFHNDLYVOWENFISRLCFYEVEVNSQTEHNFYVQEAKECNEPERFN 290
 DB 167 LTRNLNLS--EFOLELSMN--RYLDHGLEHLVQYRSDRDSWT-----EQS 208
 QY 291 VENTSCFMPGVLPDNLTVIRVIRKTKKLCYEDDKLMSNMS-----QENSGKRN 341
 DB 209 VDRHRSSTLSPVDAOKLYTFRVRSRYNPLC-GSAQHSMDWSYPIHMGSNSTKENIENPEN 267
 QY 342 STLYITMLLIVPIYVAGAILVL---LYLKRKRIIPPP 379
 DB 268 PSLFALAVLPLGSMGLIVSLICYCWLER---TMRPIP 304

RESULT 13

PRIR-RAT STANDARD; PRT: 610 AA.
 AC P05710; Q63451; Q63723; Q62832; Q64274; Q63479;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (LACTOGEN RECEPTOR).
 GN PRLR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91155946.
 RA SHIROTA M., BANVILLE D., ALI S., JOLICOEUR C., BOUTIN J.M.,
 RA EDERY M., DUANE J., KELLY P.A.;
 RT "Expression of two forms of prolactin receptor in rat ovary and
 RT liver."
 RL MOL. Endocrinol. 4:1136-1143(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (LONG FORM AND SHORT FORM).
 RP STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY;
 RX MEDLINE: 90241201.

RA ZHANG R., BYCZKO E., TSAI-MORRIS C.H., HU Z.Z., DUFAU M.L.;
 RT "Isolation and characterization of two novel rat ovarian lactogen
 RT receptor cDNA species."
 RL Biochem. Biophys. Res. Commun. 168:415-422(1990).
 PY [3]
 RP SEQUENCE OF 231-610 FROM N.A.
 RA BANVILLE D., STOCO R., MURPHY K.R., BOIE Y., KELLY P.A.;
 RL Submitted (MAR 1996) to the EMBL/GenBank/DBJ databases.
 FL [4]
 RE SEQUENCE FROM N.A. AND PARTIAL SEQUENCE (MEDIUM FORM).
 RC TISSUE-LIVER;
 RC MEDLINE: 88165059.
 RA BOUTIN J.M., JOLICOEUR C., OKAMURA H., GAGNON J., EDERY M.,
 RA SHIROTA M., BANVILLE D., DUSANTER-FOURT I., DUANE J., KELLY P.A.;
 RT "Cloning and expression of the rat prolactin receptor, a member of
 RT the growth hormone/prolactin receptor gene family."
 RL Cell 53:55-77(1988).
 RF [5]
 RP SEQUENCE FROM N.A. (FORM NB2).
 RC TISSUE-LYMPHOMA;
 RX MEDLINE: 92041834.
 RA ALI S., PELLIGRINI I., KELLY P.A.;
 RT "A prolactin-dependent immune cell line (Nb2) expresses a mutant form
 RT of prolactin receptor."
 RL J. Biol. Chem. 266:20110-20117(1991).
 RN [6]
 RP SEQUENCE FROM N.A. (FORM NB2).
 RX MEDLINE: 95014432.
 RA O'NEAL K.D., YU-LEE L.Y.;
 RT "Differential signal transduction of the short, Nb2, and long
 RT prolactin receptors. Activation of interferon regulatory factor-1 and
 RT cell proliferation."
 RL J. Biol. Chem. 269:26076-26082(1994).
 CC [1]-FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC [2]-SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC [3]-ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE PRODUCED BY ALTERNATIVE
 CC SPLICING OF THE PRLR GENE.
 CC [4]-SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC [5]-SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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FT CARBOHYD 99 99
FT CARBOHYD 127 127
FT VARSPLIC 131 150
FT VARSPLIC 151 610
FT VARSPLIC 281 310
FT VARSPLIC 311 610
FT VARSPLIC 342 539
FT CONFLICT 236 236
FT CONFLICT 345 345
FT CONFLICT 465 465
FT CONFLICT 466 466
FT CONFLICT 469 469
FT CONFLICT 541 541
FT CONFLICT 555 555
SQ SEQUENCE 610 AA: 68599 MW: C579BC43 CRC32:

POTENTIAL.
EYKOLKDKKTYLWVKSPPPT -> DYRWVSCSHQENALPKSA
KIN (IN SHORT FORM).
MISSING (IN SHORT FORM).
KXKSELLSLACQDPPPTSDDEDLLVEFL ->
TQSPSKYDLYLALPGFGFKLDNAGELDY (IN
MEDIUM FORM).
MISSING (IN MEDIUM FORM).
MISSING (IN FORM N2).
V -> A (IN REF. 2).
G -> V (IN REF. 2).
E -> K (IN REF. 1).
Q -> E (IN REF. 2).
A -> G (IN REF. 2).
T -> M (IN REF. 1).
Q -> K (IN REF. 2).

Query Match 8.1%; Score 189; DB 1; Length 610;
Best Local Similarity 23.7%; Pred. No. 3.3e-07;
Matches 68; Conservative 43; Mismatches 120; Indels 56; Gaps 10;

QY 109 KSLIVKCISSPEGDPESAVTELQCIWHLNLSYKCSWLPGRNTSPDNTLYYHRSLE 168
DB 25 KPEI--HKCRSP--DKET-----FTCMWNPGRDGLPTNYSLSYKEGK 65

QY 169 KIHOCNIFREGQFEGCSFDLTKVKDSFEQHSVOIWKDNAGKIKPSNIYPLTSRYKP 228
DB 66 TTYECDDYVTSGN--SCFP--SKQYTSIMKITYITVATNOMGSSSDPLVDVYIVBP 122

QY 229 DPP-----HIKILSEHNDLYQWENPQNFISR---CLFEYEVNNSQTEHNFYVOE 279
DB 123 EPPRNLJLEVKQKDKKTYLWVKSPPPTITDVYTGWTFMEYELRLKPEKEEHEIF-- 180

QY 280 ACCENEFERNVENTSCFNPVGLPDLTVIRIVATNKLCEYDDKLSWNSQEMSIGKK 339
DB 180 -----TGHOTQFVFYFDLYPGQKYLVOYTR-----CKPDHGYMSWQSSSEVEMP 222

QY 340 RNSLTYITMLIYPIVAGAIIVLLYLKRLK-----IIFPPIPP 381
DB 223 NDTLADTIVTIIIVALLSAVICLIWMAVALKGYSMATCIPFPVGP 269

RESULT 14
PRLR_BOVIN STANDARD: PRT; 581 AA.
AC Q28172;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM;
RX MEDLINE; 93246019.
RA SCOTT P., KESSLER M.A., SCHULER L.A.;
RT "Molecular cloning of the bovine prolactin receptor and distribution
RT of prolactin and growth hormone receptor transcripts in fetal and
RT utero-placental tissues";
RL Mol. Cell. Endocrinol. 89:47-58(1992).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC -----
CC 3MBL: L02549; AA51417.1;
CC HSSP; P14787; 1AN3.
DR PFAM; PF00041; I03; 2.
DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 24
FT CHAIN 25 581
FT DOMAIN 25 234
FT TRANSMEM 235 258
FT DOMAIN 259 581
FT DOMAIN 25 122
FT DOMAIN 123 227
FT DISULFD 36 46
FT DISULFD 75 86
FT CARBOHYD 59 59
FT CARBOHYD 132 132
SQ SEQUENCE 581 AA: 65153 MW: CDECA0A2 CRC32:

Query Match 8.0%; Score 186; DB 1; Length 581;
Best Local Similarity 24.3%; Pred. No. 5.3e-07;
Matches 80; Conservative 44; Mismatches 115; Indels 90; Gaps 16;

QY 108 EKPSILVEKCISSPEGDPESAVTELQCIWHLNLSYKCSWLPGRNTSPDNTLYYHRSLE 167
DB 29 EKPKLY--KCRSPGK-----ETTCWNEPQADGLPTNITLYTHKKE 69

QY 168 KIHOCNIFREGQFEGCSFDLTKVKDSFEQHSVOIWKDNAGKIKPSNIYPLTSRYKP 227
DB 70 TLHCEPD--YKNGPNSCF--SKKHTSIMKMYVITVANINOMGSSSDPLVDVYIVYE 126

QY 228 DPPPHKILNSF--HND-----LYQWENPQNFISRCLFEYEVNNSQTEHNFYVOE 270
DB 127 PPP--ANLTLEKHPEDKRPYLMKISPTMTDVKSGFI--IYELRLKPEKATDWE 181

QY 271 THNFVVOEAKCENPEERNVENTSCFNPVGLPDLTVIRIVATNKLCEYDDKLSWNSW 330
DB 182 THFTLKQYOLKFN-----LYPGQKYLVOIR-----CKPDHGYMSW 218

QY 331 SQEMSIGKRNSTLYITMLIYPIVAGAIIVLLYLKRLK-----IIFPPIPPGKIF 385
DB 219 SPESLIQPNDEPVDTSWIMFVALLSAVICLIWMAVALKGYSMATCIPFPVGP-RI- 277

QY 386 KEMFGQNDTILMKKYYDIY--EKOTKEE 412
DB 277 -----KGFVHLLEKGSSE 291

RESULT 15
PRLR_RABIT STANDARD: PRT; 616 AA.
AC P14787;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MAMMARY GLAND;
RX MEDLINE; 89184578.

```

Search completed: January 20, 2000, 06:19:57
 CPU time: 94 sec

RA EDERY M., JOLICOEUR C., LEVI-MEXRUBIS C., DUSANTER-FOUR I.,
 RA PETRIDOU B., BOUTIN J.M., LESUEUR L., KELLY P.A., DIANE J.,
 RT "Identification and sequence analysis of a second form of prolactin
 RT receptor by molecular cloning of complementary DNA from rabbit
 RT mammary gland.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:2112-2116(1989).
 RN [2]
 RP 3D-STRUCTURE MODELING OF 30-228.
 RX MEDLINE: 97248733.
 RA HALABY D., THOREAU E., DIANE J., MORON J.P.:
 RT "Homology modeling of rabbit prolactin hormone complexed with its
 RT receptor.";
 RL Proteins 27:459-468(1997).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb-slb.ch).
 CC -----
 DR EMBL: J04510; AAA1457.1;
 DR PIR: A30304; A30304.
 DR PDB: 1AN3; 03-DEC-97.
 DR PFAM: PF00041; fn3; 2.
 DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
 DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 616
 FT DOMAIN 25 234 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 235 258 POTENTIAL.
 FT DOMAIN 259 616 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 122 FIBRONECTIN TYPE-III.
 FT DOMAIN 124 227 FIBRONECTIN TYPE-III.
 FT DISULFID 36 46 BY SIMILARITY.
 FT DISULFID 75 86 BY SIMILARITY.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 104 104 POTENTIAL.
 FT CARBOHYD 132 132 POTENTIAL.
 SQ SEQUENCE 616 AA; 68840 MW; FB6170B1 CRC32;

Query Match 8.0%; Score 185; DB 1; Length 616;
 Best Local Similarity 27.3%; Pred. No. 6.9e-07;

Matches 80; Conservative 40; Mismatches 105; Indels 68; Gaps 17;

OY 109 KPSILVEKCSPPGDPESAATLQCIWNLSTYKCSWLPGRNTSPDNTLYLWHRSL 168
 DB 30 KPRIF--KCRSPK-----ETFTCMWRGADGGLPTNTLYL-HKEGE 69
 OY 169 KI-HQENIFREGQYFGCSFDLTKVDSFEQSVQIMVADNKGKIKPSNIYPLTSRK 227
 DB 70 TITHECPD-YKTGGPNSCYF--SKKHTSIWTIITIVNATNMGSSVSDPRYDVYIIVE 126
 OY 228 PDPPIKNSLF--HNDD---LYVOMENQNTISR---CLFYEV---NNSQETHN 273
 DB 127 PDPPI--VNLTLEVKHPEDRKPYLWAKLPPTLVDSGWLTLQYELIKPKAKAEMETH- 184
 OY 274 VEVYQAKCENPFEKREVENTSCFVWPGVLPDLNTVRIKTKNKLCYEDDKLMSNWSQ 333
 DB 184 -FAGQQTQ-----FKILSLYPGQKYLQVR-----CKPDHGFMSWMSPE 221
 OY 334 MSIGKRNSTLY-ITMLLYPVI--VAGATVLLYLKRLKI--TFPPYDP 381
 DB 222 SSIOINDEFTWIDTWFVAVLSTIICLIIMWAVALKGYSWTCIFPPVGP 274

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 20, 2000, 06:37:46 ; Search time 24.34 Seconds
(without alignments)
1074.609 Million cell updates/sec

Title: US-09-077-817-4
Perfect score: 2324
Sequence: 1 MEMPARLCGLMALLCAGCG.....QTKETDSVVLIENTKKASQ 427

Scoring table: BLOSUM62

Searched: 199794 seqs, 61255205 residues

Database : SPTREMBL_1.1:*

word size : 0

Number of hits that pass the threshold : 199794

- ```

1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.potent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

```

**Pred. No.** is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

| Result | Query | Score | Match | Length | DB     | ID                       | Description |
|--------|-------|-------|-------|--------|--------|--------------------------|-------------|
| No.    |       |       |       |        |        |                          |             |
| 1      | 2288  | 98.5  | 427   | 4      | 095646 | 095646 homo sapien       |             |
| 2      | 1610  | 69.3  | 349   | 6      | 097597 | 097597 bos taurus        |             |
| 3      | 294.5 | 12.7  | 430   | 4      | 014633 | 014633 homo sapien       |             |
| 4      | 287.5 | 12.4  | 383   | 11     | 088786 | 088786 mus musculi       |             |
| 5      | 282.5 | 12.2  | 396   | 4      | 014631 | 014631 homo sapien       |             |
| 6      | 279.5 | 12.0  | 415   | 11     | 0920K4 | 0920K4 cavia porc        |             |
| 7      | 229   | 9.9   | 335   | 4      | 013469 | 013469 homo sapien       |             |
| 8      | 221.5 | 9.5   | 410   | 4      | 014431 | 014431 homo sapien       |             |
| 9      | 182   | 7.8   | 296   | 6      | 018880 | 018880 bos taurus        |             |
| 10     | 177   | 7.6   | 346   | 13     | 093404 | 093404 oreochromis       |             |
| 11     | 175   | 7.5   | 581   | 6      | 046561 | 046561 ovis aries        |             |
| 12     | 169.5 | 7.3   | 422   | 4      | 075462 | 075462 homo sapien       |             |
| 13     | 164   | 7.1   | 881   | 13     | 057519 | 057519 xenopus laevis    |             |
| 14     | 162.5 | 7.0   | 333   | 4      | 016564 | 016564 homo sapien       |             |
| 15     | 154.5 | 6.6   | 896   | 11     | 061446 | 061446 rattus norvegicus |             |
| 16     | 148.5 | 6.4   | 1093  | 11     | 070535 | 070535 rattus norvegicus |             |
| 17     | 146   | 6.3   | 634   | 6      | 046600 | 046600 bos taurus        |             |
| 18     | 132   | 5.7   | 217   | 6      | 046386 | 046386 mus musculus      |             |
| 19     | 130   | 5.6   | 206   | 4      | 016354 | 016354 homo sapien       |             |
| 20     | 128   | 5.5   | 890   | 11     | 0921A0 | 0921A0 cavia porcellus   |             |
| 21     | 127   | 5.5   | 830   | 11     | 063257 | 063257 rattus norvegicus |             |
| 22     | 126.5 | 5.4   | 335   | 6      | F79203 | F79203 ovis aries        |             |
| 23     | 123.5 | 5.3   | 1471  | 5      | 018245 | 018245 caenorhabditis    |             |
| 24     | 119.5 | 5.1   | 140   | 4      | 014632 | 014632 homo sapien       |             |
| 25     | 115.5 | 5.0   | 979   | 4      | 099650 | 099650 homo sapien       |             |

## ALIGNMENTS

|    |        |     |       |    |                     |
|----|--------|-----|-------|----|---------------------|
| 26 | 1.15   | 4.9 | 981   | 13 | 013146              |
| 27 | 1.14.5 | 4.9 | 233   | 4  | C002027             |
| 28 | 1.14   | 4.9 | 13055 | 5  | O09165              |
| 29 | 1.13.5 | 4.9 | 4868  | 13 | Q91319              |
| 30 | 1.14   | 4.8 | 467   | 11 | Q63216              |
| 31 | 108.5  | 4.7 | 500   | 5  | O94655              |
| 32 | 106.5  | 4.6 | 500   | 5  | O15770              |
| 33 | 106    | 4.6 | 1825  | 5  | O61210              |
| 34 | 105.5  | 4.6 | 1177  | 4  | Q13221              |
| 35 | 103.5  | 4.5 | 198   | 6  | O18985              |
| 36 | 104.5  | 4.5 | 2214  | 4  | O92856              |
| 37 | 101.5  | 4.5 | 584   | 13 | O98921              |
| 38 | 104.5  | 4.5 | 626   | 13 | O98922              |
| 39 | 104.5  | 4.5 | 504   | 13 | O98923              |
| 40 | 104    | 4.5 | 456   | 5  | Q25242              |
| 41 | 104    | 4.5 | 480   | 5  | O25241              |
| 42 | 104    | 4.5 | 971   | 11 | O70458              |
| 43 | 104    | 4.5 | 970   | 11 | O88821              |
| 44 | 103.5  | 4.5 | 1019  | 5  | O96435              |
| 45 | 103    | 4.4 | 1118  | 4  | Q15426              |
|    |        |     |       |    |                     |
|    |        |     |       |    | 013146 brachydan    |
|    |        |     |       |    | 0002027 homo saplen |
|    |        |     |       |    | Q09165 caenorhabd1  |
|    |        |     |       |    | Q91319 rana catesb  |
|    |        |     |       |    | Q63216 rattus norv  |
|    |        |     |       |    | O94655 plasmodium   |
|    |        |     |       |    | O15770 plasmodium   |
|    |        |     |       |    | O61210 caenorhabd1  |
|    |        |     |       |    | Q13221 homo saplen  |
|    |        |     |       |    | O18985 cervus elap  |
|    |        |     |       |    | O92856 homo saplen  |
|    |        |     |       |    | O98921 gallus gail1 |
|    |        |     |       |    | O98922 gallus gail1 |
|    |        |     |       |    | O98923 gallus gail1 |
|    |        |     |       |    | Q25242 lucilia cup  |
|    |        |     |       |    | Q25241 lucilia cup  |
|    |        |     |       |    | O70458 mus musculu  |
|    |        |     |       |    | O88821 mus musculu  |
|    |        |     |       |    | O96435 drosophila   |
|    |        |     |       |    | Q15426 homo saplen  |

|        |                                                                                                               |              |
|--------|---------------------------------------------------------------------------------------------------------------|--------------|
| RESULT | 1                                                                                                             |              |
| C95646 |                                                                                                               |              |
| ID     | 095646                                                                                                        | PRELIMINARY; |
| IC     | 095646;                                                                                                       | PRT; 427 AA. |
| DT     | 01-MAY-1999 (TEMBREL. 10, Created)                                                                            |              |
| DT     | 01-MAY-1999 (TEMBREL. 10, Last sequence update)                                                               |              |
| DT     | 01-MAY-1999 (TEMBREL. 10, Last annotation update)                                                             |              |
| DE     | INTERLEUKIN-13 RECEPTOR.                                                                                      |              |
| OS     | Homo sapiens (human)                                                                                          |              |
| OC     | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Placentalia; Homiidae; Homidae; Homo. |              |
| CC     | [1]                                                                                                           |              |
| PP     | SEQUENCE FROM N.A..                                                                                           |              |
| RA     | MORIMASA W.; TERIMASA H.;                                                                                     |              |
| WT     | Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases                                                        |              |
| DR     | EMBL; U08379; AAD00530.1.                                                                                     |              |
| SC     | Receptor.                                                                                                     |              |
| SN     | SEQUENCE: 427 AA; 48779 MW; BED0274E CRC32;                                                                   |              |

|                       |              |                    |              |            |
|-----------------------|--------------|--------------------|--------------|------------|
| Only Match            | 98.5%        | Score 2288         | DB 4         | Length 427 |
| Best Local Similarity | 98.6%        | Pred. No. 2.4e-192 |              |            |
| Matches 421           | Conservative | 0                  | Mismatches 6 | Indels 0   |
|                       |              |                    |              | Gaps 0     |

  

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| QY | 1   | MEMPARLCGAMALLLCAGGGGGGGAAPETQPTNLNLSVENLCITYATWMPPEGASS     | 60  |
|    |     |                                                              |     |
| Db | 1   | MEMARFCGAMALLLCAGGGGGGGAAPETQPTNLNLSVENLCITYATWMPPEGASS      | 60  |
|    |     |                                                              |     |
| QY | 61  | NCSJWFSHRGDKQDKRIAPETRRLSEVPLNERICLQVSGCSTNESKPSILVEKCISP    | 120 |
|    |     |                                                              |     |
| Db | 61  | NCSJWFSHRGDKQDKRIAPETRRLSEVPLNERICLQVSGCSTNESKPSILVEKCISP    | 120 |
|    |     |                                                              |     |
| QY | 121 | PEPSPESAVTELOCIMHNLSTYKMCMSLPGRNTSPDNTNTLYYHMRSLKIHQCENIFREG | 180 |
|    |     |                                                              |     |
| Db | 121 | PEGPESAVTELOCIMHNLSTYKMCMSLPGRNTSPDNTNTLYYHMRSLKIHQCENIFREG  | 180 |
|    |     |                                                              |     |
| QY | 181 | CYFSCSFDTLKYVDSSEFQHSVOIWKNDAGIKRSENVLPETLSRVKPDPHIKNLSFHN   | 240 |
|    |     |                                                              |     |
| Db | 181 | CYFSCSFDTLKYVDSSEFQHSVOIWKNDAGIKRSENVLPETLSRVKPDPHIKNLSFHN   | 240 |
|    |     |                                                              |     |
| QY | 241 | DLTYQWENQONFISCLFEYEYVNNNSQFETHNVYVQEAECENDEPERNENTSCMP      | 300 |
|    |     |                                                              |     |
| Db | 241 | DLTYQWENQONFISCLFEYEYVNNNSQFETHNVYVQEAECENDEPERNENTSCMP      | 300 |
|    |     |                                                              |     |
| QY | 301 | GVLPDLTNTYRIKVKTNKLCYEDDKLMSWMSQEMSIGKRNRSTYITMLLVPYIVAGAI   | 360 |
|    |     |                                                              |     |
| Db | 301 | GVLPDLTNTYRIKVKTNKLCYEDDKLMSWMSQEMSIGKRNRSTYITMLLVPYIVAGAI   | 360 |
|    |     |                                                              |     |

QY 361 IYLLLYLKLKIIIPPPIDPGKIFEMFGDONDDTLHMKKYDIYEKOTKEETDSVLLIE 420  
 DB 361 IYLLLYLKLKIIIPPPIDPGKIFEMFGDONDDTLHMKKYDIYEKOTKEETDSVLLIE 420  
 QY 421 NUKRASQ 427  
 DB 421 NUKRASQ 427

## RESULT 2

097597 PRELIMINARY: PRT: 349 AA.

AC 097597  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (FRAGMENT).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;  
 OC Bovinae; Bos.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TRIGONA W.L., HIRANO A., BROWN W.C., ESTES D.M.;  
 RT "Biological Activities of Interleukin-13 on bovine lymphocytes:  
 RT Implications for signaling through IL-13R $\alpha$ 1."  
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF074402; AAC98147.1;  
 KW Receptor.  
 FT NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 349 AA: 39644 MW; AB48B972 CRC32;

Query Match 69.3%; Score 1610; DB 6; Length 349;  
 Best Local Similarity 84.5%; Pred. No. 3.9e-133;  
 Matches 293; Conservative 17; Mismatches 37; Indels 0; Gaps 0;

QY 35 VTNLSVSENICTVITWNPPEGASNCSLMYFSHFGDKODKRIAPETRSIEVPLNERI 94  
 DB 1 VTNLSVSENICTVITWNPPEGASNCSLMYFSHFGDKODKRIAPETRSIEVPLNERI 60  
 QY 95 CLQVSOCSSTNSEKPSILYEKICSPEDPSAVATELOCIMHNSYKCSWLPGRNTSP 154  
 DB 61 CLQVSOCSSTNSEKPSILYEKICSPEDPSAVATELOCIMHNSYKCSWLPGRNTSP 120  
 QY 155 DNTYLYYHRSLEKIHOCENIFREGOYGCSPDLTKVDSSEHOSVQIMKDNAGKIT 214  
 DB 121 DNTYLYYHRSLEKIHOCENIFREGOYGCSPDLTKVDSSEHOSVQIMKDNAGKIT 180  
 QY 215 PSFNIVPLTSRVKPPPHIKNLFSHNDLYVQWENPQNFISRCLEFEVEVNNSTETNAV 274  
 DB 181 PSFNIVPLTSRVKPPPHIKNLFSHNDLYVQWENPQNFISRCLEFEVEVNNSTETNAV 240  
 QY 275 FYVOAKCENPEFERNVENTSCFMPGVLPDLNLYVRIKYNKLCYEDDKLMSWSQMA 334  
 DB 241 FYVOAKCENPEFERNVENTSCFMPGVLPDLNLYVRIKYNKLCYEDDKLMSWSQMA 300  
 QY 335 SIGKRNSLTLYITMLLYVYAGAIYVLLYLKRLKIIFPPIDPGK 383  
 DB 301 SIGKRNSLTLYITMLLYVYAGAIYVLLYLKRLKIIFPPIDPGK 349

RESULT 3  
 ID 014633 PRELIMINARY: PRT: 420 AA.  
 AC 014633  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE INTERLEUKIN-5 RECEPTOR PRECURSOR.  
 GN HSTL5R.  
 OS Homo sapiens (Human);

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PERIPHERAL BLOOD.  
 RX MEDLINE: 92121815.  
 RA MURATA Y., TAKAKI S., MIGITA M., KIKUCHI Y., TOMINAGA A., TAKATSU K.;  
 RT "Molecular cloning and expression of the human interleukin 5  
 RT receptor."  
 RL J. Exp. Med. 175:341-351(1992).  
 DR EMBL: X61176; CAA43483.1;  
 KW Signal.  
 FT SIGNAL  
 FT CHAIN  
 SQ SEQUENCE 420 AA: 47670 MW; 247AB980 CRC32;

Query Match 12.7%; Score 294.5; DB 4; Length 420;  
 Best Local Similarity 24.8%; Pred. No. 6e-18;  
 Matches 102; Conservative 65; Mismatches 180; Indels 65; Gaps 16;

QY 33 PVTNLSVSENICTVITWNPPEGASNCSLMYFSHFGDKODKRIAPETRSIEVPLN 91  
 DB 32 PVTNLSVSENICTVITWNPPEGASNCSLMYFSHFGDKODKRIAPETRSIEVPLN 82  
 QY 92 ERICQV-----GSQCSSTNSEKPSILYEKICSPEDPSAVATELOCIMHNL--- 140  
 DB 83 ERICQV-----GSQCSSTNSEKPSILYEKICSPEDPSAVATELOCIMHNL--- 142  
 QY 140 -----SY--MKCSWLPGRNTSPDNTYLYYHRSLEKIHOCENIFRE--GQYRCSDDL 189  
 DB 143 YSRLRSYGVSLHCTVLVGTDAPEDTQYFLYRYSWTE--ECQYRCSDDLRLNIAQWPPR 200  
 QY 130 TKVKDSFEHOSVQIMKDNAGKITPSFNIVPLTSRVKPPPHIKNLFSHNDLYVQWEN 249  
 DB 201 TKVKDSFEHOSVQIMKDNAGKITPSFNIVPLTSRVKPPPHIKNLFSHNDLYVQWEN 260  
 QY 250 PON-FISRCLEFEVEVNNSTETNAVYVOAKCENPEFERNVENTSCFMPGVLPDLN 308  
 DB 261 PVSAPRHCPEDEYEVNHTNRG-----YLOIEKLMNTNFIISIDLSY----- 305  
 QY 309 TYRKYKYNKLCYEDDKLMSWSQMSIGKRNSTLYITMLLYVYAGAIYVLLYLK 368  
 DB 305 DVQVAAVSSMCKREAG-LMSEMSPYIYVGNDEHKLPLREMFYIVIMATICTILLISLICK 363  
 QY 369 --RLKIIFPPIDPGKIFEMFGDONDDTLHMKKYDIYEKOTKEETDSVYL 418  
 DB 364 ICHLWIKFPPIDPGKIFEMFGDONDDTLHMKKYDIYEKOTKEETDSVYL 404

RESULT 4  
 ID 088786 PRELIMINARY: PRT: 383 AA.  
 AC 088786  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DE IL-13 RECEPTOR ALPHA 2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-C3H/HEJ; TISSUE-THYMS.  
 RX MEDLINE: 98391042.  
 RA DONALDSON D.D., WHITTEN M.J., FITZ L., NEBEN T.Y., FINNERTY H.,  
 RA HENDERSON S.L., O'HARA R.M., JR., BEIER D.R., TURNER K.J., WOOD C.R.,  
 RA COLLINS M.;  
 RT "The murine IL-13 receptor alpha 2: molecular cloning,  
 RT characterization, and comparison with murine IL-13 receptor alpha  
 RT 1."  
 RL J. Immunol. 161:2317-2324(1998).  
 DR EMBL: U65747; AAC33240.1;



Db 349 ILLIFFLCRIYHMTKMPYPAPKSTFKDLIMTNT-----CEKAGSSETEIE 397  
 Oy 417 VL 418  
 Db 398 VI 399

## RESULT 7

015469 PRELIMINARY: PRT: 333 AA.  
 AC 015469;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)  
 DE SOLUBLE INTERLEUKIN-5 RECEPTOR PRECURSOR.  
 GN HS15R4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PERIPHERAL BLOOD;  
 RX MEDLINE: 92121815.  
 RA MURATA Y., TAKAKI S., MIGITA M., KIKUCHI Y., TOMINAGA A., TAKANISU K.;  
 RT "Molecular cloning and expression of the human interleukin 5  
 receptor";  
 RL J. Exp. Med. 175:341-351(1992).  
 DR EMBL: X62156; CAA44081.1;  
 KW Signal.  
 FT SIGNAL. 1 20 POTENTIAL.  
 FT CHAIN 21 333 SOLUBLE INTERLEUKIN-5 RECEPTOR.  
 SQ SEQUENCE 333 AA: 37722 MW; E86A7792 CRC32;

Query Match 9.5%; Score 229; DB 4; Length 333;  
 Best Local Similarity 24.5%; Pred. No. 2.4e-12;

Matches 81; Conservative 52; Mismatches 145; Indels 52; Gaps 14;

Oy 33 PPTNLVSVENLCTVITWMP-PEGASSNCSLWTFSHRGDKQKRIAPETRRSIEVPLN 91  
 Db 32 PVV-NFTIKVTGLAVLQWKNRPNQEQNVNLEY-----QVKNINPK-EDDETERT 82  
 Oy 92 ERICQV-----GSCSTINSEKPSILVEKICIS-----PPGDPESAATVLOCIMHNL--- 140  
 Db 83 ESKCVTILHKGPSASVRIITLQNDHSILASVNASAEIHAAPGSPGISVNLCTTTTTEDN 142  
 Oy 140 -----SY---MKCSWLPGRNTSPDNTLYYHRSLEKIHOCENIFRE--GOYFGCSFDL 189  
 Db 143 YSRLSYOVSLHCTWLVGTIDAPEDTOYFLYRYGSWTE--ECOEYSKDTLGNINACWEPFR 200  
 Oy 190 TKVKDSFEQHSVOIWMKNACKIRPSFNIVPLTSRVKPDPPHINLSFHNDLYVOMEN 249  
 Db 201 TILISKGDMVLAVLVNGSSSKSHAIRPDQLFALHAIIDQINPLANTALEGTRLSIQWEX 260  
 Oy 250 PON-FISCLPFEVAVNNSQETIHANVFYQEKACENPEPERAVENTSCMPVGVLPDILN 308  
 Db 261 PVSAPRHCDFEYVNIHNTFRNG-----YLOEKLMTNFIISIDLSKY----- 305  
 Oy 309 TVRIRKTNKLCYEDDKLMSNMSQMSIGK 338  
 Db 305 DVQVRAAVSSMKREAG-LMSEMSQPIYYGK 333

## RESULT 8

014431 PRELIMINARY: PRT: 410 AA.  
 ID 014431;  
 AC 014431;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)  
 DE GM-CSF RECEPTOR.  
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91352066.  
 RA CROSTIER K.E., WONG G.G., MATHIEY-PREVOT B., NATHAN D.G., STEFF C.A.;  
 RT "A functional isoform of the human granulocyte/macrophage  
 colony-stimulating factor receptor has an unusual cytoplasmic  
 domain";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:7744-7748(1991).  
 DR EMBL: M64445; AAA35908.1;  
 KW Transmembrane.  
 SQ SEQUENCE 410 AA: 46901 MW; 30CE1609 CRC32;

Query Match 9.5%; Score 221.5; DB 4; Length 410;  
 Best Local Similarity 22.4%; Pred. No. 1.4e-11;  
 Matches 88; Conservative 75; Mismatches 178; Indels 51; Gaps 17;

Oy 31 TOPPTNLVSVENLCTVITWMP-PEGAS-SNCSLWTFSHRGDKQKRIAPETRRSIEVP 89  
 Db 29 TVAPASSLVNTRDSR-TNLSMDQCENTFSKFL-----TDKKNRYVEERLSNNECSC 81  
 Oy 90 LNERICLOVGSOCSTINSEKPSILVEKICISPPGDPESAATVLOCIMHNSYMKCSWLP 149  
 Db 82 TFEELCHEGVTFEYHVTNSQGFQOKLLYPNSGEGTAQNFSCFIYNADLMCTVARG 141  
 Oy 150 RNTSPDNTLYYHRSLEKIHOCENIFRE--GOYFGCSFD-LTKVKDSFEQHSVOIWK 207  
 Db 142 PTPRPDVOYFLIRNSKRREIRCPYIQQDSGTHVGHCLDLSGLTSKNY-----FLVN 195  
 Oy 208 DNAGIKRPF--NIVPLTSRVKPDPPHINLSFHNDLYVOMENPQNF--ISRCLF-YEV 262  
 Db 196 GTSREIGIOFDSLDITDKIKETFNPSNVTVRCNTTCHLVWKKQPRTYOKLSYLDFOYOL 255  
 Oy 263 EVN--NSQETIHANVFYQEKACENPEPERAVENTSCMPVGVLPDILTVNIRKTNKLC 320  
 Db 256 DVHRRNTPGTENLLINVSGLENR-----XNPSSEPRAKSHVIRADVAEIL 304  
 Oy 321 YEDDLMSNMSQMSIGKRNS--TLVYTMLLIVPVIYAGALIVLYLKRLKI-TIPP 377  
 Db 305 N-----WSWSEALIEFGSDDNLGSVYIYVLLVIGTLVCG--IVLGFLEKRLRIQRLEFP 358  
 Oy 378 IP-----DPKIFKEFNGQNDLHWKRY 402  
 Db 359 VPQIKDKLNDHVEDEW-GPQRHRCGMNLY 389

## RESULT 9

018880 PRELIMINARY: PRT: 296 AA.  
 ID 018880;  
 AC 018880;  
 DT 01-JAN-1998 (TREMblrel. 05, Created)  
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)  
 DE PROLACTIN RECEPTOR SHORT FORM.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 97375450.  
 RA SCHULER L.A., NAGEL R.J., GAO J., HORSEMAN N.D., KESSLER M.A.;  
 RT "Prolactin receptor heterogeneity in bovine fetal and maternal  
 tissues";  
 RL Endocrinology 138:3187-3194(1997).  
 DR EMBL: AF027403; AAB83999.1;  
 DR FEMM: PF00041; fn3.2.  
 SQ SEQUENCE 296 AA: 33854 MW; 8B40CCD8 CRC32;

Query Match 7.8%; Score 182; DB 6; Length 296;

Best Local Similarity 24.3%, Prec. No. 2.7e-08;  
Matches 72; Conservative 41; Mismatches 111; Indels 72; Gaps 13;

OY 108 EXPSTIVEKICSPGDEPSATTELQCIWHLNLSYKCSWLPGRNTSPDNTNTLYWHRSL 167  
DB 29 EKPRLV--KCRSPGK-----EFTTCWEPGADGLPTNTLYTKRGE 69  
OY 168 EKHOCENIFREGOYFGSFDLTWKDSSFEQHSQVQIMKDNAGKIKPSFNIPLTSRYK 227  
DB 70 TLHRCPD-YKRGNSCF--SKHTSIWKMYVITVANAINGMSSDPLVHTYIYE 126  
OY 228 PDPRIKULSF--HND--LYQWENP--FISRCLEYEVANNST--E 270  
DB 127 PEPP--ANLTLELKHEDRKPILMIKSPPTMTDVKSGWFI--IQYEIRLKEKATDWE 181  
OY 271 THNVYVOAKENPEFEENVENTSCFMPVGLPDTLNTVRIRVKTNKICYEDDKLMSW 330  
DB 182 THFTLKQOLKIFN-----LYPGOKYLVQIR-----CKPDHGYSWM 218  
OY 331 SOEMSGKRNSTLYTMLIVPVIAGAIIVLLYLKRLK-----IIFPIPP 381  
DB 219 SPESIOIPNDPVPVDTSMITFVALISAVICIMWAVALKGYSMTCTILPVPGP 274

## RESULT 10

O93404

AC 093404

PRELIMINARY: PRT: 346 AA.

DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)  
DE PROLACTIN RECEPTOR (FRAGMENT).  
OS Oreochochomus mossambicus (Mozambique tilapia) (Tilapia mossambicus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
CC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;  
OC Perciformes; Labroidae; Cichlidae; Tilapia.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-GILL;  
RA SHIRAIISHI K., MATSUDA M., MORI T., TETSUYA H.;  
RT "Expression of prolactin and cortisol receptor gene in early-life  
stages of tilapia (Oreochochomus mossambicus)."  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF080247; AAC31825.1;  
DR PFM: PF00041; fn3; 2.  
FT NON-TER 346  
SQ SEQUENCE 346 AA; 39203 MM; 1E8A63B9 CRC32;

Query Match 7.6%, Score 177; DB 13; Length 346;

Best Local Similarity 22.4%, Pred. No. 8.9e-08;  
Matches 64; Conservative 40; Mismatches 104; Indels 78; Gaps 11;

OY 130 TELQCIWHLNLSYKCSWLPGRNTSPDNTNTLYWHRSLKIKHOCENIFREGOYFGSFDL 189  
DB 33 TEITCRSEPEKFTCMWPKPSDGLPTLYALYKREGSDVHPCDYHAKGN-SCFEN- 91  
OY 190 TKVKSSEFQHSQVQIMKDNAGKIKPSFNIPLTSRYKPDPRHINKLSHND--LYV 245  
DB 91 -KNDTLIWSVITVAVNALGKITYSDPYDIOVYIVKHPPEKLEVITMKQGPFLRV 149  
OY 246 QWENPONTISR--CLFEYEV--NNSQTEH--NFFVOEAKENPEFER 289  
DB 150 SWEPHKKADTRGKWTILYELAVKLEDESEENNAAGQKFNIFSLRSG----- 201  
OY 230 NVENTSCFMPVGLPDTLNTVRIRVKTNKICYEDDKLMSWQSGKRNSTLYITM- 349  
DB 201 -----GTYLIVR-----CKPDHGYSWM-----STSVKVP 228  
OY 349 -----LLIVPVIAGAIIVLLYLK-----KRLKIIIFPIPP 381  
DB 229 AYLHREKSWILVYVSAFILLILILMIOMNSHLKCHLCPVPGP 274

## RESULT 11

O46561

AC 046561

PRELIMINARY: PRT: 581 AA.

DT 01-JUN-1978 (TREMBlrel. 06, Created)  
DT 01-JUN-1993 (TREMBlrel. 06, Last sequence update)  
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)  
DE PROLACTIN RECEPTOR LONG FORM PRECURSOR.  
OS Ovis aries (sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
CC Euteria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;  
OC Caprine; Ovis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 98001468.  
RA BIGSON C., BINART N., ORMANDY C., SCHULER L.A., KELLY P.A.,  
RJ DJIANE J.;  
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning  
and genomic analysis reveal that the two forms arise by different  
alternative splicing mechanisms in ruminants and in rodents."  
RJ J. Mol. Endocrinol. 19:109-120(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA BIGSON C., DJIANE J.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DE EMBL: AF041257; AAB96795.1;  
DR PFM: PF00041; fn3; 2.  
RN Signal.  
RT SIGNAL  
FT CHAIN 1 24 POTENTIAL.  
SQ SEQUENCE 581 AA; 65235 MM; 6792A7C7 CRC32;

Query Match 7.5%, Score 175; DB 6; Length 581;

Best Local Similarity 23.8%, Pred. No. 2.6e-07;  
Matches 78; Conservative 46; Mismatches 116; Indels 88; Gaps 16;

OY 108 EXPSTIVEKICSPGDEPSATTELQCIWHLNLSYKCSWLPGRNTSPDNTNTLYWHRSL 167  
DB 29 EKPRLV--KCRSPGK-----EFTTCWEPGADGLPTNTLYTKRGE 69  
OY 168 EKHOCENIFREGOYFGSFDLTWKDSSFEQHSQVQIMKDNAGKIKPSFNIPLTSRYK 227  
DB 70 TLHRCPD-YKRGNSCF--SKHTSIWKMYVITVANAINGMSSDPLVHTYIYE 126  
OY 228 PDPRIKULSF--HND--LYQWENP--FISRCLEYEVANNST--ET 271  
DB 127 PEPP--ANLTLELKHEDRKPILMIKSPPTMTDVKSGWFI--IQYEIRLKEKATDWE 182  
OY 272 HNVYVOAKENPEFEENVENTSCFMPVGLPDTLNTVRIRVKTNKICYEDDKLMSW 331  
DB 182 HNP--KNDTLIWSVITVAVNALGKITYSDPYDIOVYIVKHPPEKLEVITMKQGPFLRV 219  
OY 332 QWENPONTISR--CLFEYEV--NNSQTEH--NFFVOEAKENPEFER 289  
DB 220 PSF--QWENPONTISR--CLFEYEV--NNSQTEH--NFFVOEAKENPEFER 289  
OY 387 EMEGDNDTILMKRYDIY--EKOTKEE 412  
DB 277 -----KGFIDHLEKRSSE 291

## RESULT 12

O75462

AC 075462

PRELIMINARY: PRT: 422 AA.

DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)  
DE CYTOKINE-LIKE FACTOR-1 PRECURSOR.  
GR CLF-1.  
OY Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA ELSON G.C.A., GRABER P., LOSBERGER P., HERREN S., GREYNER D.,  
 RA MONOD L.N., WELLS T.N.C., KOSCO-VILBOIS M.H., GAUCHAT J.F.;  
 RT "GLF-1, a Novel Soluble Protein Shares Homology with Members of the  
 RT Cytokine Type-I Receptor Family";  
 RL J. Immunol. 0:0-0(1998).  
 DR EMBL: AF059293; AAC2835.1;  
 DR PRAM: PF00041; fn3; 2.  
 KW Signal.  
 FT SIGNAL 1 37 POTENTIAL.  
 FT CHAIN 38 422 CYTOKINE-LIKE FACTOR-1.  
 SQ SEQUENCE 422 AA; 46301 MW; 8779BC9 CRC32;

Query Match 7.38; Score 169.5; DB 4; Length 422;  
 Best Local Similarity 22.58; Pred. No. 5.2e-07;  
 Matches 80; Conservative 53; Mismatches 159; Indels 63; Gaps 18;  
 QY 13 LLLAGG---GGGGGAAPTEPTPTNLSVENVICTVITWNPPEGASNCISLWFSH 69  
 DB 24 LLLCVLGPAPGSAHRAVISPPDPTLLIGSLATCSV---HGDPGATAGLWTLN- 80  
 QY 70 FGDKODKIAETRRSIEVPLNERICLV---SGOCSTNE---SEKPSILVEKICSP 120  
 DB 80 -----GRLPELRSVLNA---STLALALANLSRSGNLVCHANDGSLGSCLY- 131  
 QY 121 PEGPESAVTELOCIMHNSLTKSCWLFGRN--TSPDTNTLYLWHSLEKIHOCENIFR 178  
 DB 131 -VGPRPEKPVNISCMKMKDLTCRMTPGAGETFLHTNYSILKRLWYGDONNCEERT 189  
 QY 179 EGOFGCSFDLTAKVD--SFEQHSQVIMVKNAGIKRSPINIVPLTSVYKRDPP--HIK 234  
 DB 190 VGP-SCHIP---KDLALFTPEIWEATNRLSASADVTLLDLVYTTDPPDVHVS 244  
 QY 235 NLSFHNLDLYQWENP---QNFISRCLE---YEVEVNSQTEHNVFVQAKCENPEFE 288  
 DB 245 RVGLLEQGLSVRSPALNDFLFOAKQIRYVEDSDVMKVVDDY----- 291  
 QY 289 RNVENTSCFVPGVLPDTLNTVRIRVTKNKLCEYEDK--LMSNMSQESICKKN 341  
 DB 291 --SNQTSCLAGLKPGLVYFVQVRCNPFGL--YGSKKAGIWEWSHPYASTPRS 341

RESULT 13  
 057519  
 ID 057519 PRELIMINARY; PRT: 881 AA.  
 AC 057519;  
 DT 01-JUN-1998 (Tremblrel. 06, Created)  
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
 DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)  
 DE GEL30P1.  
 GN XGP130.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;  
 OC Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae; Xenopodinae;  
 OC Xenopus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA CHEN J., GRACE A., CHEN K.R.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF041845; AAC03531.1;  
 DR PRAM: PF00041; fn3; 4  
 SQ SEQUENCE 881 AA; 99003 MW; 647E152E CRC32;

Query Match 7.18; Score 164; DB 13; Length 881;  
 Best Local Similarity 25.38; Pred. No. 4.1e-06;  
 Matches 56; Conservative 32; Mismatches 81; Indels 58; Gaps 10;  
 QY 123 GDPESAVTELOCIMHNSLTKSCWLFGRNTPDTNTLYL--YWHRSLEKIHOCENIFREGO 181

DB 119 GLPDKPTNLTCLAYVNDNLTCTWDPGRPTNLTPTNLTLSHRW-----A 161  
 QY 182 YFGCSFDLTAKVKSFEQHS-----VOIMVNDKIKRSPINIVPLTSVYKRDPP 231  
 DB 162 HFGANY--CGGANNSTHSPGFQFYDTTFQVEANTELQSELTLPVAVKPNP 219  
 QY 232 H---INLSFHNLDLYQWENPQNFISRCLEFEVEVNSQTEHNVFY--VOEAKCENP 285  
 DB 220 QLSLLISLSPN-ALKIEKNP-----ITNAPNLKYNIRYRPVKTQDMEMV 265  
 QY 286 EFERVENTSCFVPGVLPDTLNTVRIRVTKNKLCEYED--KIMSNQO 332  
 DB 266 PEEDTASHPDSFTLQDILLPTVVEVSIR-----CIHKDGHGFWSDMSE 308  
 RESULT 14  
 016564  
 ID 016564 PRELIMINARY; PRT: 333 AA.  
 AC 016564;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)  
 DE GM-CSF RECEPTOR PRECURSOR.  
 OC Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91376112.  
 RA RAINES M.A., LIU L., QUAN S.G., JOE V., DIPERSIO J.F., GOLDE D.W.;  
 RT "Identification and molecular cloning of a soluble human  
 RT granulocyte-macrophage colony-stimulating factor receptor";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8203-8207(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PLACENTA;  
 RX MEDLINE: 91088339.  
 RA ASHWORTH A., KRAFT A.;  
 RT "Cloning of a potentially soluble receptor for human GM-CSF";  
 RL Nucleic Acids Res. 18:7178-7178(1990).  
 DR EMBL: W73832; AAA35909.1;  
 DR EMBL: X54935; CAA38697.1;  
 KW Signal: Alternative splicing.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 333 GM-CSF RECEPTOR.  
 SQ SEQUENCE 333 AA; 38438 MW; 48178079 CRC32;

Query Match 7.08; Score 162.5; DB 4; Length 333;  
 Best Local Similarity 20.58; Pred. No. 1.6e-06;  
 Matches 65; Conservative 61; Mismatches 152; Indels 39; Gaps 12;  
 QY 31 TQPTNLSVENVICTVITWNPPEGAS--SNCSLWFSHFGKODKIAETRRSIEVP 89  
 DB 29 TVAPASLLNRFDSR--TNLSMDCQENTFTSKCFL-----TDKKNVYVPRLSNNECSC 81  
 QY 90 INERICQVQSQCSTNSEKPSILVEKICSPPEGDPESAVTELOCIMHNSLTKSCWLP 149  
 DB 82 TFEICLHEGVTEVHVNTSQRGFOQLTPNSGREGTAQNFSCFLYNDLNCWTWARG 141  
 QY 150 RNTSPDTNTLYLWHSLEKIHOCENIFRE--GOYFGCSFP-LTKVKSFEQHSVOIMV 207  
 DB 142 PTAPRDVQFLYIRNSKRREINCPYIYQDSGTHVGHLDNLSGLTSRNY-----FLVN 195  
 QY 208 DNAGKIRPSP--NIVPLTSVYKRDPPHIKNLSFHNLDLYQWENPQNF--ISRCLE-YEV 262  
 DB 196 GTSREICIQFDSLDLTKKIEREPNSVNTVRCNTHTCLVRMKOPRYOKLSYLDFOYOL 255  
 QY 263 EVN--NSQTEHNVFYQVQAKCENPEERVENTSCFVPGVLPDTLNTVRIRVTKNKL 320  
 DB 256 DVHRKNYQPTGENTLLNVSGDLENR-----YNPSSSEPRAKHSVIRAAADVRL 304

OY 321 YEDDKLMSNSQMSIG 337  
 DB 305 N-----WSSWSEAIERFG 316

RESULT 15

O64146 PRELIMINARY: PRT; 896 AA.  
 ID O64146  
 AC O64146;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, last annotation update)  
 DE INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).  
 GN RIL-3R<BETA>.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 95370942.  
 RA APPEL K., BUTTINI M., SAUTER A., GEBICKE-HARTER P.J.;  
 RT "Cloning of rat interleukin-3 receptor beta-subunit from cultured  
 RT microglia and its mRNA expression in vivo."  
 RL J. Neurosci. 15:5809-5809 (1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-WISTAR; TISSUE-BRAIN;  
 RA GEBICKE-HARTER P.J.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; S79263; AAB35068.1; .  
 DR EMBL; AJ000555; CAA04186.1; .  
 DR PFAAM; PF00041; fn3; 2.  
 KW Signal.  
 FT NON\_TER 1 1  
 FT NON\_TER 896 896  
 SQ SEQUENCE 896 AA; 99504 MW; 8E7ED2CD CRC32;

Query Match 6.6%; Score 154.5; DB 11; Length 896;  
 Best Local Similarity 24.2%; Pred. No. 2.8e-05;  
 Matches 86; Conservative 53; Mismatches 140; Indels 77; Gaps 20;

OY 51 TNNPPEGASS--NCSLMYSHFGDKQDKIAPTRRSIEVPLNERICLOYSQSCSTNESE 108  
 DB 184 SW---EDASSLHNCMLV-----TLEPKLFLP---NSTIV-ARYRAQLAPGSSLSGRPSG 231  
 OY 109 -KSLIVEKCSPPEDGPEASVATELOCIMHNLSTYMKCSMLPGKNTSPDTNYTLYYHRL 167  
 DB 232 WSEPEVHMD--SPTF--DKARPONLQCFEDGIQSLNCSMEVWTWTVDSVSGLFYSSSPK 286  
 OY 168 EKHOCENIFREGO-----YFGCSFDLTWKDSSFEHSHSQIMVKNDAKIKPSFNVPL 222  
 DB 287 AGEKKCSPPYKELQASRYTRYHCSLNV--DPAHSQYTVSV-RLKQGFISFN---- 340  
 OY 223 TSRAKDPPIHKNLSFHNLDLYQWENPQNFISRCLEYEVENSQTEHNVFYVEAK- 282  
 DB 340 --HIQNNPPTL-NLTKNRPSYSLHWETQK-----MSYPFIQHAFOVQYKKK 382  
 OY 282 ---CENPEPERNVENTSCFVPGVLPDITLVIRYKTKNKLCTYEDDKLMSNSQMSIGK 338  
 DB 383 LDMWESKTE-NLNHAHSMDLPLEPTSYCAVRYKT--IPEYKGLWSEWSENECTW-- 437  
 OY 339 KRSTLYITMFLVPIYVAGAIIVLLYL-----KRLKTIIFPIPPGK 383  
 DB 437 ---TIDWVPTLWIVLIVLFLILFLALRFQCIYGCILYRRWK---EKIPNPSK 485

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ORIGIN

Query Match 100.0%; Score 4009; DB 5; Length 4009;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4009; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tcaacccgagccggcgctcccgagcgagagagcgctgcatgagtgagcgcgcgcttcgagg 60
DB 1 tcaacccgagccggcgctcccgagcgagagcgctgcatgagtgagcgcgcgcttcgagg 60
QY 61 ctgtggcgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 120
DB 61 ctgtggcgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 120
QY 121 gaaactagccacccctgagcaaatgtagtgctgctgctgctgctgctgctgctgctgctg 180
DB 121 gaaactagccacccctgagcaaatgtagtgctgctgctgctgctgctgctgctgctgctg 180
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DB 841 gagcacataatgtttctcagctcaagagagctaaatgltgagaaatccagaattggagaga 900
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QY 1501 ttgagagagagtgag 1560
DB 1501 ttgagagagagtgag 1560
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DB 1621 tccgagagagctacttacttcttcttcttcttcttcttcttcttcttcttcttcttctt 1680
QY 1681 agggagacatcttggagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 1740
DB 1681 agggagacatcttggagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 1740
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QY 1861 caattggagagtcgag 1920
DB 1861 caattggagagtcgag 1920
QY 1921 caaaatgag 1980
DB 1921 caaaatgag 1980
QY 1981 tgccttaaccagacttctgag 2040
DB 1981 tgccttaaccagacttctgag 2040
```

|    |       |                                                                 |       |
|----|-------|-----------------------------------------------------------------|-------|
| Db | 1981  | TGCGTGAATCCACAGTACTCGGGAAAGCTGAGCGACGATGAATTGTTGAACCTGGAGAGT    | 204.0 |
| Qy | 204.1 | ggagagctgcagtgagcgagaaatcaacacacgtgacctctgctggtgtgacagagaagac   | 2100  |
| Db | 204.1 | GGAGAGTTCGAGTGCAGAGATATCACACCACTGACACTGTAGCTGGGTGCACAGCAACAC    | 2100  |
| Qy | 210.1 | tcgtctcaaaaaaacaacaacaacaacaacaacaacaacacttcaatcttcgaggt        | 2160  |
| Db | 210.1 | TCGTCTCAAAAAACAACAACAACAACAACAACAACAACCTCTTAATATTCGGAGT         | 2160  |
| Qy | 216.1 | catcatccctcttcagacagcaatttcctctgcttctgaagccccagaaatcagltgttgcc  | 2220  |
| Db | 216.1 | CATCATTCCTCCCTTGACAGACATTTTCCCTGCTTGAAGCCCCAGAAATCAGTGTGGCC     | 2220  |
| Qy | 222.1 | atgatgacaactacagaaaaaacaagagcagctctcttgcagaaccttcaagacat        | 2280  |
| Db | 222.1 | ATGATGACAACTACAGAAAAACCAAGAGCGACTTCTTCCCAAGACCTTCCAAACCAAT      | 2280  |
| Qy | 228.1 | tttagagctgttagggcgatggaggtagaatgacatcccttggtgatttagagttcaacag   | 2340  |
| Db | 228.1 | TTAGAGCTGTAGGGCGATGGAGGTGAATGACTCCTTGAGTATTAAGATTTCAACCAATG     | 2340  |
| Qy | 234.1 | aagctctcaacaagtaattctctcacactctgtcactcaagtagacattactgtgctt      | 2400  |
| Db | 234.1 | AAGCTCTCAACAAGTATTTTCTTCAACCTGTGACTCAAGTAGATTTACTGTTCTTT        | 2400  |
| Qy | 240.1 | ggtttgtgctagggccccgggtgtgaaagcagagaccccttccaggggtttacagtcatt    | 2460  |
| Db | 240.1 | GGTTTGTGCTAGGGCCCCGGGTGTGAAGCACAGACCCCTCCAGGGGTTTACAGCTATTT     | 2460  |
| Qy | 246.1 | tgaagacccctcaagctctctgcacatttttttaactctcaacagatatttttagact      | 2520  |
| Db | 246.1 | TGAAGACTCTCAGTCTCTTGACACTTTTTTTTAATCTCCACAGCATTTTCAGACT         | 2520  |
| Qy | 252.1 | tttaacctccctaattccaacaacgfatccccctttgtcatactccctccctccctct      | 2580  |
| Db | 252.1 | TTTAACCTCCTAATTCACACAGTATTOCCCTTTTGCACTTCCTCCTTCCTTCCTT         | 2580  |
| Qy | 258.1 | gtagcccttctgaccttcaatctggaatagagatlaaactctgctcagagagacctgtgagag | 2640  |
| Db | 258.1 | GTAGCCCTTTCACCTTCTCATTTGGAATTAGAGATTAATCTGCTCAGAGACCTCGAGAG     | 2640  |
| Qy | 264.1 | cagggagataatgcatctcaagtttaagtggtgagtaactctggaaaaacaatgactaattct | 2700  |
| Db | 264.1 | CAGAGGATTAATTACACATCTAGGTTAAGTGTGATGTGAGAAACAATGTCAATTTCT       | 2700  |
| Qy | 270.1 | tgcataatttgaactcccatgtcgaggggtttcagacattgatatgttcatcttctaa      | 2760  |
| Db | 270.1 | TGCATATTTTGTAACTTCCATGTGAGGGTTTTCAGCATTTGATTTTGTCATTTCTTAA      | 2760  |
| Qy | 276.1 | cagagatgaggtgtglatcttcacgctgaacatgtgatctgcgtctgagaaaaaagaatag   | 2820  |
| Db | 276.1 | CAGAGATGAGGTGTATCTTCAGGTAGAACATGTGATTCGCTTGAGAAAAAAGATAG        | 2820  |
| Qy | 282.1 | ttgaaactatcttctctcttcttaacaagatvggtgccagagatcccttctctcgccataa   | 2880  |
| Db | 282.1 | TTGAACTATTTCTCTTCTTTCACAGATGGGCCAGGATCCTCTTCTCTCGCCATTA         | 2880  |
| Qy | 288.1 | atgatttaataaagcttttgcctcttaacattggtgagccagacagcagagctctgttt     | 2940  |
| Db | 288.1 | ATGATTAAATTAAGCTTTTGTGTCTTACATTGGTAGCCAGCCAGCAAGCTCTGTGTT       | 2940  |
| Qy | 294.1 | atgctttcttgaggggacatalatgtggttccatcttcacacctacacacaacatctcgat   | 3000  |
| Db | 294.1 | ATGCTTTGGGGGGCATATATGTGGTTCCATCTCAGCTATCCACACAAATATCCGAT        | 3000  |
| Qy | 300.1 | ataaccctctactcttactcttcccccaaattaagaaglatatggaaatgagagcatct     | 3060  |
| Db | 300.1 | ATAACCTCTACTCTTACTTCTTCCCAAAATTTAAAGATATGCGAAATGAGACGACATTT     | 3060  |
| Qy | 306.1 | cccccaacccatctctctctcaacaacagagccatattactggtgagagacttggaaact    | 3120  |
| Db | 306.1 | CCCCAACCCATTTCTCTCTCAACACAGCATCATTTACTGTGTAAGAACTTGGAACT        | 3120  |

|                 |                                                               |                                                                   |                      |
|-----------------|---------------------------------------------------------------|-------------------------------------------------------------------|----------------------|
| Cy              | 3121                                                          | tatttcacagctcttccaaacctttaccatcatatbttaaataatgatgcatcttgcaat      | 3180                 |
| Tb              | 3121                                                          | TTATTTCGAAAGTGTCTCAAAACATTTAACCAATATTAATAAAGAAGCATTTGGCAAT        | 3180                 |
| Oy              | 3181                                                          | tcctgcaccttagggggagggaagaataagaaacctcactctcacaggttgttgtaacaagt    | 3240                 |
| Dh              | 3181                                                          | TCCTGCCTCCTTAGGGGAAGGGAGATAGAAACCCTCACCTCTACAGGTTTTGGTACAAGT      | 3240                 |
| Oy              | 3241                                                          | ggcaacctgtctccaaggccgtgtagaagcaatgtgtgccctgtctcttgaggaaactgtg     | 3300                 |
| Dh              | 3241                                                          | GCGAACCTGCTCCATCGGCCGTGTAAACCAAGTGAGCCCTGGCTCTCTGTAGCAAGCTGG      | 3300                 |
| Oy              | 3301                                                          | ggttcctajaaaatygcagatgtraaatltttcttiiaaafccaattgaaagcctggagaaagac | 3360                 |
| Dh              | 3301                                                          | GGTTCATGACCAATGGCAGATGTAAACTTATCTCTGAATCAATGTAGAGCTGGGGACAGC      | 3360                 |
| Oy              | 3361                                                          | cctgtgtagatgttctaacttgtctgcctgtctctcagaagaatatltgtgtttctcgt       | 3420                 |
| Dh              | 3361                                                          | CCGTAGTAAAGTGTCTACTTGTGTGCGTGTCTGTAGAAAATATTGGTTTTCCGT            | 3420                 |
| Oy              | 3421                                                          | ataagaaatgagatuaatctcttcacaggtatttatattccttggaaagcaaacaccatgc     | 3480                 |
| Dh              | 3421                                                          | ATAGGAATGAGATTAATCTCTCCAGATATTTTAAATTCGGACAAACCAACCATATGC         | 3480                 |
| Oy              | 3481                                                          | ctccccttagccatltttactgtatcatccattagaatggccatgaagagagatgtcgtaaa    | 3540                 |
| Dh              | 3481                                                          | CTCCCCCTAGCCATTTTACTGTATTNCCATTTTAAATGAGCCATGAAGAGATGCTGTGAA      | 3540                 |
| Oy              | 3541                                                          | atccccacaacaactgtatgtctgacagticaltgcaatctgtggagtgaggaaatgtacttt   | 3600                 |
| Fb              | 3541                                                          | ATTCGCAACAACATTTGATGCTGACAGTCATGCAGTACGTGGAGTGGGAAGTATCTTTT       | 3600                 |
| Oy              | 3601                                                          | gttcccatctctcttcttttagcagtaaatagctgaagggaagaaagggaagaaaggaagt     | 3660                 |
| Dh              | 3601                                                          | GTTCGCAATCCTCTCTCTTTTAGCAGTAAATTAAGCTGAGGAAAAAGGAGAAAGGAAGT       | 3660                 |
| Oy              | 3661                                                          | tatgggaataaccgtgtgtgtgtgtgaacctagtgcttbgggagctcttggaggtgtctgt     | 3720                 |
| Dh              | 3661                                                          | TATGGGAATACCTGTGTGTGTGTGATCCCTAGGCTTGTGGAGGTCTGT                  | 3720                 |
| Oy              | 3721                                                          | atcagtggaattcccatcccccgtgtggaaataagtagaggctcaattactgttttagtcta    | 3780                 |
| Dh              | 3721                                                          | ATCAGTGGATTTCCCATCCCCTGTGGGAATTAGTAGGCTCATTTACGTTTTAGGCTTA        | 3780                 |
| Oy              | 3781                                                          | gccatgttgatlttttttctctaataatacctaagaacaaaccagtgtcagaaatgtatctct   | 3840                 |
| Dh              | 3781                                                          | GCCATGTGATTTTTTCCTAATATACCTTAACCAAAACCAGTGTAGGATGTATATCTT         | 3840                 |
| Oy              | 3841                                                          | atctcttcgttcaagtaagtttttccctcacctcagtcagcaataaggagatagtgtaaaca    | 3900                 |
| Dh              | 3841                                                          | ATCTTTCGTTCACTTAAGTTTTTCCCTTCACTGCGCACAGTAAGGATATGTCAAACA         | 3900                 |
| Oy              | 3901                                                          | tgttaacattttgtgtagttcttcaaccaaggaatgtttctgtttaactctctataaggaa     | 3960                 |
| Fb              | 3901                                                          | TGTTAAATTTTGTGTAGCTTTCAACCAAGGAGATGTTCTGTTTAACTTCTTATAGCAA        | 3960                 |
| Oy              | 3961                                                          | gcttgataaataataatatgtctttttgtatgtacccaataaaaaaa 4009              |                      |
| Dh              | 3961                                                          | GCTTGATTAATAATTAATATGTTCTTTTGTATGTACCCCAAAAAAAAA 4009             |                      |
| <b>RESULT 2</b> |                                                               |                                                                   |                      |
| Locus           | HSLI3RAL                                                      | 3999 bp                                                           | mRNA PRI 2c-FEB-1997 |
| DEFINITION      | H.sapiens mRNA for IL13 receptor alpha-1 chain.               |                                                                   |                      |
| Accession       | Y09338                                                        |                                                                   |                      |
| NID             | 9185307                                                       |                                                                   |                      |
| VERSION         | YC9328.1 GI:1885307                                           |                                                                   |                      |
| KEYWORDS        | alpha 1 chain; IL13RA1 gene; Interleukin-13 receptor.         |                                                                   |                      |
| SOURCE          | human                                                         |                                                                   |                      |
| ORGANISM        | Homo sapiens                                                  |                                                                   |                      |
|                 | Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; |                                                                   |                      |





QY 3721 atcagtgattcccccctctgaggaaatagtaggtcattcctgttttaagtcctc 3780  
 Db 3721 ATCAGTGGATTTCOCATCCCTGTGGAAATAGTAGGCATTTACTGTTAGTCTCA 3780  
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 Db 3901 TGTAAACATTTTGGTAGCTTCAACAGGATGTTCTGTTAACCTTCTATAGGAA 3960  
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 Db 3961 GCTTGAGTAAATAATATGCTTTTGTATGTACCC 3999

RESULT 3  
 HSIL13RA  
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 DEFINITION Y10659  
 ACCESSION Y10659  
 NID G1806035  
 VERSION Y10659.1 GI:1806035  
 KEYWORDS IL13ra gene; Interleukin-13.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominoidea; Homo.

REFERENCE  
 AUTHORS Gauchat, J.F.M., Schlagenhauf, F., Feng, N.P., Moser, R., Yamage, M.,  
 Jeanmin, P., Aouani, S., Elson, G., Notarangelo, L.D., Wells, T.,  
 Eugster, H.P. and Bonnefoy, J.Y.  
 TITLE A novel 4 kb IL-13ra mRNA expressed in human B, T and endothelial  
 cells, encoding for an alternate type two IL-4/IL-13R  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 4039)  
 AUTHORS Gauchat, J.F.M.  
 JOURNAL Direct Submission  
 TITLE Submitted (20-JAN-1997) J-F.M. Gauchat, Geneva Biomedical Research  
 Institute, Immunology, Glaxo Research And Development, 14 Ch Des  
 Aux, Plan-Les-Quatre, CH1228, SWITZERLAND  
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 STNSEKRSILVERKISPPEDPEASVTEICIAHNSIWKCSMLGKNTSPDNTL  
 IVPLTSRKPDPPHILKLSFNDLYVQWNPONLSRCIFYEVENNSOTENHNVEY  
 VQAKCNPEPERVENTSCFVPGVLPDLNTRVIRVYTNKLCYEDDKLTSMNSQEM  
 SIGKRSSTLYITLILVPIVAGAILVLLILKRLKIIIFPIPDPKIFEMGDO  
 NDDTLHKKTDITKOTKEETDSVLIENLKRSQ"

BASE COUNT 1135 a 839 c 896 g 1169 t  
 ORIGIN  
 Query Match 99.7%; Score 3995; DB 9; Length 4039;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 cagccggccctgctccagagcgagagctgagtagtgccggcgctctcgagc 61  
 Db 12 CAGCCGGCCCTGCTCCAGAGCGAGAGCTGAGTAGTGCCTCGCGCTCGCGGCG 71  
 QY 62 tggggcgctgctgctgctggcgcgagcgggcgggcgggcgggcgggcgggcg 121  
 Db 72 TGGGGCGCTGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTACGG 131  
 QY 122 aaactcagccactgtgcaaatctgagtgctgctgttgaacacctcgcagtaatat 181  
 Db 132 AAACTCACCCACCTGTGACAAATTTGAGTGTCTGTGAAAACCTCTGCACAGTAATAT 191  
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 QY 962 tcagaataagagtcacaaacaaataagttatgtatgagatgacaaactctgagtaatt 1021

Db 972 TCAGATTAAGAGTCAAAACAAATAGTATGCTATGAGATGACAAACTGAGATAAT 1031  
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 Db 1032 GGACCCAAAGAAATAGATATAGTAAGAGCGCAATTCACACTACATACCAAGATTAC 1091  
 Qy 1082 tcatgtgtccagtcacgctcgcaagctgcaatcatagtaactccgtgttcaactaaagac 1141  
 Db 1092 TCATTGTTCCAGTATCGTCCAGAGTCGCAATCATATGATCTCTGCTTACCTAAAAAGC 1151  
 Qy 1142 tcaagattatatactccctcccaattccctgtaacctgcaagaattttaagaatgtttg 1201  
 Db 1152 TCAAGATTATATATATCCCTCCCAATCTGATCCGCAAGATTCTTAAAGAAATGTTG 1211  
 Qy 1202 gagcccaagaatagatgatactctgcaactggaagaagtaagatactctatagaagaacca 1261  
 Db 1212 GAGACCAAGAAATGATGATCTGCACTGGAAGAAATACGACATCTATGAGAAAGCAACA 1271  
 Qy 1262 agagggaaacgcactctgtagtgctgataagaacctaagaagccctcagtgatga 1321  
 Db 1272 AGGAGAAACCGACTCTGTATGCTGATGATAAACTGAGAAAGCCTCTCAGTATGGA 1331  
 Qy 1322 gataattatcttaactcactgtagccttgagaagaattctcccatctccatgtgt 1381  
 Db 1332 GATAATTTATTTTACCTTCACTGACCTTGAGAAAGATCTCCCATCTCCATTTGTT 1391  
 Qy 1382 atctgggaactataatgaagaactgaactactgcaactttaaaaaagggagcca 1441  
 Db 1392 ATCTGGGAATCTTATTAATGAAACTGAAACTACGACCAATTTAAAAAGCGAGCTCA 1451  
 Qy 1442 taagaagcaagctctatgtatgtgagtcgcaagcaaaataaataatgagcgctt 1501  
 Db 1452 TAAAGCCACAGGCTTTATATGTAAGTCCGACCGAAAAATAAATAATGAGCGCTT 1511  
 Qy 1502 tggagaagagtgtagagtcattctcatgaattataaaagccagagcttcaactag 1561  
 Db 1512 TGGAGAGAGAGTGGAGCATCTCATGAAATTAATAAAGCAGAGCTTCAAACTAGG 1571  
 Qy 1562 ggaaaaagcaaaagtgaatgtatgtgtgagttactcttcaagaattgtgaact 1621  
 Db 1572 GGACAAAGCAAAAAGTATGATAGTGTGAGTAAATCTTCAAGAAATTTGACAACTT 1631  
 Qy 1622 cctgagagatcatcactgctgtgttctgttctgttcaactgaacttaatttttta 1681  
 Db 1632 CCTAGGAGATCATACTGCTTGTGTCTTGTCTGTCACATGAAATTTATTTTATA 1691  
 Qy 1682 ggggaactcattggtgtgcaaatgtaagtcaaaacttgatgcacaaagaacatgata 1741  
 Db 1692 GGGGAGACTCATTTGGGGTCAAAATGCTAATGTCAAACTTGAGTCAAAAGAACATGTAGA 1751  
 Qy 1742 aaaaaaatgataaataatctgatatgtatgtttgggactctatgaacctgtttggg 1801  
 Db 1752 AAAAATAATGATTAATAATCTATATGTAATGTTGGGATCTTATGAAACATGTTTGAG 1811  
 Qy 1802 ctactaaacactttaaacaagctcgagctggtgtcggtgctcaagcctgtaactccagc 1861  
 Db 1812 CTATTAAACCTTTTAACACTCTGCGCTGGCTCGGCTGCTCAGCGCTGTAATCCAGC 1871  
 Qy 1862 aatttggagtcgagggcgagctgcaactcagagtgcaagagttccagacagcctgacc 1921  
 Db 1872 AATTGGGAGTCCAGAGGGGCGGATCCTGAGGTGAGGAGTTCCAAACACAGCCTGACC 1931  
 Qy 1922 aaatgtgtgaactcctcctactaaactacaaaaataactggtgtgtgtgagcgt 1981  
 Db 1932 AAAATGGGAAACCTCCTCTTACTAAATACAAATAATTAACATGGGTGTGGTGGCGGT 1991  
 Qy 1982 gccgttaactccagctactcgaggaagctgagcgagtgtaattgtttgaactcgtggagtg 2041  
 Db 1992 GCGTGTATATCCAGCTACTCGGGAAGCTGAGGAGCGTAATTTGTTGAACCTGGGAGGTG 2051  
 Qy 2042 gaggttcagtgagcagagatcacacacacgtaactcagcctgggtgacagagcaagact 2101

Db 2052 GAGGTTTCAGTGAGAGATCACACCACTGCACTTACGCTGGGTGACAGCAAGACT 2111  
 Qy 2102 ctgtttaaadaaacaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaac 2161  
 Db 2112 CTGCTTAATAAACAATAAACAATAAACAATAAACAATAAACAATAAACAATAAACAATAA 2171  
 Qy 2162 atcttccctctcgagaaattctcctctgtcttgaagaagcccaagaatactgttggcca 2221  
 Db 2172 ATCATTTCCCTTGACAGATTTTCTGCTTGAAGGCCAGAAATCAGATGTGGCA 2231  
 Qy 2222 tga+g+caactacagaacaaacagagagcagctcttggccaaagccttcaagccatt 2281  
 Db 2232 TGATCAACATCAAGAAAAACAGAGGAGCAGCTTTTGGCAAGACCTTCAAAAGCATTT 2291  
 Qy 2282 tggc+tgtagggagagtgagtagaattgactccttgggttgaagttgaagttcaacata 2341  
 Db 2292 TAGCTGTAGGGGAGATGAGAGGTAGAAATGACTCTTGAGATTAGAGTTTAACACATA 2351  
 Qy 2342 agcct+taacaatgtaattctctcactcctgtaactcaagtagcaattactgtcttg 2401  
 Db 2352 AGCTCTAACAATGATATTTTCTACCTGCTACTCAAGTAGCATTTACTGTGCTTTG 2411  
 Qy 2402 gtt+tgctagggc+ccgggggtgta+gcaacagacccttccaggggttcaagttatt 2461  
 Db 2412 GTTGTGTAGGCCCCGGGAGTGAAGCACAGACCCCTCCAGGGGTTTACAGTATTT 2471  
 Qy 2462 gagactcctgaagttcttccacttttttttaactccacagatcatttccaaact 2521  
 Db 2472 GAGACTCCTCAGTTCTTCCACTTTTATTTTAACTCCACAGTATTTTACAGACTT 2531  
 Qy 2522 ttaactcctcaatccacaactgtaattccctcttggcatctccctcctcctctg 2581  
 Db 2532 TTAATCCTCAATTTCCACACAGATTTCCCTTTGCAATTCCTCCTCCTCCTCCTG 2591  
 Qy 2582 tagccttttgaacttcaatggaatlagatgataatctgctcaagagagcctgagagc 2641  
 Db 2592 TAGCTTTGACTTTCAATGGAATTAAGATGTAATCTGCTCAGAGACCTGGAGAGC 2651  
 Qy 2642 agaggaatlaagacatccaggttaagtgtagtaactggaacaaatgaataattct 2701  
 Db 2652 AGAGATATTTGACATCTCAGGTTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2711  
 Qy 2702 gcatatt+gtaactcctcagtgagaggtttcaagatgataattgtgcatctcctaac 2761  
 Db 2712 GCATTTTGTATCTTCATGATGAGGTTTTCAGATGATGATTTGTGATTTTGAAC 2771  
 Qy 2762 agagatg+ggtgtaactcctcagtagaacaattgtaattcgttgaagaaagaatagt 2821  
 Db 2772 AGAGATGAGGTGATCTTCACAGTGAACATTTGATTTGCTTGAGAAAAAGAAATAGT 2831  
 Qy 2822 tgaacatctctctcttctttaaagaatgagtgagaggttccctcttctcgcataaa 2881  
 Db 2832 TGAACCTAATTTCTCTTTTAAAGATGGTCCAGATTCCTCTTCTCGCATATA 2891  
 Qy 2882 tgaatcaataaagactttgtgtcttcaatgtagagcaagcagagctggttta 2941  
 Db 2892 TGATTAATTAATATCTTTGTGTCTTACATTTGTAAGCAGACCAAGAGCTGTGTTA 2951  
 Qy 2942 tgc+tttgggggcaatattgggttccattctcaacttccacaacaataatccgtata 3001  
 Db 2952 TGCTTTTGGGGGCAATATTTGGGTTTCATTTCTACCTATCCACACAACATATCCGATA 3011  
 Qy 3002 taf+ccctactcttacttccccaatttaagaagatgaggaagagagcattc 3061  
 Db 3012 TATCTCTTCTTACTTCTCCCAATTTAAAGATGTGGAAATGAGGAGGATTTT 3071  
 Qy 3062 cccg+cccatctctcctcacaacagacatcattactgttgaacttgagaact 3121  
 Db 3072 CCGCACGC+ATTTCCTCTCTCAGACAGACTCATATTTACTGTGGAAGTGAAGACTT 3131  
 Qy 3122 catt+caagttgttcaaacatttcaacaatcaatlaataacaa+gagtcatttgcatt 3181  
 Db 3132 TATTCCAAAGTTTCAAAACATTTTCAATCATATTATATACATATGATCTATTGCAATT 3191







|    |      |                                                                  |      |
|----|------|------------------------------------------------------------------|------|
| OY | 482  | ggaatccagcgcgcgacacactatactctcactattggcagagaagccctggaaaaa        | 541  |
| Db | 489  | ggaatpccagcgcgcgacacactatctctcactattggcagagaagccctggaaaaa        | 548  |
| OY | 542  | ttcatcaatgfganaaacattcttagaagaagccaactcttggtcttccttgcctga        | 601  |
| Db | 549  | ttcatpcaatgfgaanaaacattcttagaagaagccaactcttggtcttccttgcctga      | 608  |
| OY | 602  | ccaaatgfaaggaatccagttcttgaacacacagctgccaaataatggtcaagataatg      | 661  |
| Db | 609  | ccaaatgfaaggaatccagttcttgaacacacagctgccaaataatggtcaagataatg      | 668  |
| OY | 662  | caggaaaaattnaaacccctctcaatatagtgaccttaactcccgtyfgaactgtac        | 721  |
| Db | 669  | caggaaaaattnaaacccctctcaatatagtgaccttaactcccgtyfgaactgtac        | 728  |
| OY | 722  | ctccacatataaanaacctctccctccacacatgatagtacctataatgtycfaatgysgaatc | 781  |
| Db | 729  | ctccacatataaanaacctctccctccacacatgatagtacctataatgtycfaatgysgaatc | 788  |
| OY | 782  | cacgaatttatatagaagtgaccttttatagaataagtcataataacacgaactg          | 841  |
| Db | 789  | cacgaatttatatagaagtgaccttttatagaataagtcataataacacgaactg          | 848  |
| OY | 842  | agacacataatgcttctcctcagcccaagaggtctaaatgtyagaaatccgaatttgaaga    | 901  |
| Db | 849  | agacacataatgcttctcctcagcccaagaggtctaaatgtyagaaatccgaatttgaaga    | 908  |
| OY | 902  | atgtyggaataacatctgttctcaatggtccctgtygttcttcctgatactttgaacaag     | 961  |
| Db | 909  | atgtyggaataacatctgttctcaatggtccctgtygttcttcctgatactttgaacaag     | 968  |
| OY | 962  | tcaaatataagtgtaaaaaacaataaagtctatgctcataggaatgacaacactggaataat   | 1021 |
| Db | 969  | tcaaatataagtgtaaaaaacaataaagtctatgctcataggaatgacaacactggaataat   | 1028 |
| OY | 1022 | ggagccaaagaatgagatagtgtaagaagcgaattcccaactctacataaccatgcttac     | 1081 |
| Db | 1029 | ggagccaaagaatgagatagtgtaagaagcgaattcccaactctacataaccatgcttac     | 1088 |
| OY | 1082 | tcattgttccagatcatgctggcaggtgcaactatagtaactcctgcttacccttaaaaaagc  | 1141 |
| Db | 1089 | tcattgttccagatcatgctggcaggtgcaactatagtaactcctgcttacccttaaaaaagc  | 1148 |
| OY | 1142 | tcaagatathataatctccctccaattccctgatactctgycgaagatltttaaagaatgttg  | 1201 |
| Db | 1149 | tcaagatathataatctccctccaattccctgatactctgycgaagatltttaaagaatgttg  | 1208 |
| OY | 1202 | gagagccgaatagatgatacctctgacctcggagaagaatgaagaatctctatggaagcaacca | 1261 |
| Db | 1209 | gagagccgaatagatgatacctctgacctcggagaagaatgaagaatctctatggaagcaacca | 1268 |
| OY | 1262 | aggaaggaacacgactctgtatgctgtatgaanaaacctggaagaagccctcagtatgta     | 1321 |
| Db | 1269 | aggaaggaacacgactctgtatgctgtatgaanaaacctggaagaagccctcagtatgta     | 1328 |
| OY | 1332 | gataattatttcaacttccactgtgaccttgagaagatcttcccatctcccatgtgtc       | 1381 |
| Db | 1339 | gataattatttcaacttccactgtgaccttgagaagatcttcccatctcccatgtgtc       | 1388 |
| OY | 1382 | atctgggaactatataatggaacatgaactactgcacatttaaaacagcgagcca          | 1441 |
| Db | 1389 | atctgggaactatataatggaacatgaactactgcacatttaaaacagcgagcca          | 1448 |
| OY | 1442 | taagaagccacagctcttattgtgtgagtcgcgcacgaaanaacataatgtyggcgctt      | 1501 |
| Db | 1449 | taagaagccacagctcttattgtgtgagtcgcgcacgaaanaacataatgtyggcgctt      | 1508 |
| OY | 1502 | tggaagaagaatgtyggaatcaattctatgataataaagcagaggtttaaactgtg         | 1561 |
| Db | 1509 | tggaagaagaatgtyggaatcaattctatgataataaagcagaggtttaaactgtg         | 1568 |

|                                                            |                                                                          |                                                            |                      |
|------------------------------------------------------------|--------------------------------------------------------------------------|------------------------------------------------------------|----------------------|
| CY                                                         | 1562                                                                     | Ggacaaagcaaaaztgatgatgaatggcgaggatcaattcatcaaggtttgacaactt | 1621                 |
| L*                                                         | 1563                                                                     | GGACAAAGC/PNAAATGTATGATAGTGGTGACTTAATTATTCAGSAGTTGTGACAATT | 1628                 |
| OY                                                         | 1622                                                                     | cctggaggatcataccttgcttggtgttccttggtgcacaatgacaatttatgtta   | 1681                 |
| D*                                                         | 1629                                                                     | CCTGGAGGATCATACTTGCTTGCTTCTTGCTGCACAATGAACAATTTATTATTGTA   | 1688                 |
| OY                                                         | 1682                                                                     | ggggaactaatctgggg                                          | 1698                 |
| DB                                                         | 1689                                                                     | GGGGAACATCATTTGGGG                                         | 1705                 |
| RESULT                                                     | 5                                                                        |                                                            |                      |
| ASU62858                                                   |                                                                          |                                                            |                      |
| LOCUS                                                      | HS062858                                                                 | 1572 bp                                                    | mRNA PRI 30-NOV-1996 |
| DEFINITION                                                 | Human interleukin-13 receptor mRNA, complete cds.                        |                                                            |                      |
| ACCESSION                                                  | U62858.                                                                  |                                                            |                      |
| NID                                                        | gi:695375                                                                |                                                            |                      |
| VERSION                                                    | U62858.1                                                                 | GI:1695875                                                 |                      |
| KEYWORDS                                                   |                                                                          |                                                            |                      |
| SOURCE                                                     | human:                                                                   |                                                            |                      |
| ORGANISM                                                   | Homo sapiens:                                                            |                                                            |                      |
| REFERENCE                                                  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;            |                                                            |                      |
| AUTHORS                                                    | Euthalia, Primates; Cetarthrin; Homnidae; Homo.                          |                                                            |                      |
| TITLE                                                      | Anan,M.J., Tayebi,N., Obidi,N.I., Puril,R.K., Modi,W.S. and Leonard,W.J. |                                                            |                      |
| JOURNAL                                                    | CDNA cloning and characterization of the human Interleukin-13            |                                                            |                      |
| REFERENCE                                                  | receptor alpha chain                                                     |                                                            |                      |
| AUTHORS                                                    | . Biol. Chem. (1996) In press                                            |                                                            |                      |
| TITLE                                                      | 2 (bases 1 to 1572)                                                      |                                                            |                      |
| JOURNAL                                                    | Amann,M.J., Tayebi,N., Modi,W.S. and Leonard,W.J.                        |                                                            |                      |
| FEATURES                                                   | Submitted (02-JUL-1996) Lab. of Molecular Immunology, NHLBI, NIH,        |                                                            |                      |
| SOURCE                                                     | 9000 Rockville Pike, Bethesda, MD 20892-1674, USA                        |                                                            |                      |
| LOCATION/Qualifiers                                        |                                                                          |                                                            |                      |
| 1..1572                                                    |                                                                          |                                                            |                      |
| /organism="Homo sapiens"                                   |                                                                          |                                                            |                      |
| /db_xref="taxon:9606"                                      |                                                                          |                                                            |                      |
| /chromosome="X"                                            |                                                                          |                                                            |                      |
| 85..1368                                                   |                                                                          |                                                            |                      |
| /function="cytokine receptor"                              |                                                                          |                                                            |                      |
| /note="IL-13 receptor; IL-13R or IL-13Ralpha; this protein |                                                                          |                                                            |                      |
| together with the 140 kDa IL-4 binding protein, IL-4R or   |                                                                          |                                                            |                      |
| IL-Ralpha, can form a functional receptor for IL-13;       |                                                                          |                                                            |                      |
| IL-13R plus IL-4R is also one of the functional forms of   |                                                                          |                                                            |                      |
| the IL-4 receptor, the other is IL-4R plus the common      |                                                                          |                                                            |                      |
| cytokine receptor gamma chain"                             |                                                                          |                                                            |                      |
| /codon_start=1                                             |                                                                          |                                                            |                      |
| /product="interleukin-13 receptor"                         |                                                                          |                                                            |                      |
| /protein_id="AA837127.1"                                   |                                                                          |                                                            |                      |
| /db_xref="PID:g1695876"                                    |                                                                          |                                                            |                      |
| /db_xref="GI:1695876"                                      |                                                                          |                                                            |                      |
| /translation="MEMPARLCIGMALLLAGGGGGGAAPETTOPPVTLSSVEN      |                                                                          |                                                            |                      |
| LCPTITWNPPEGASSNCSLWFSEFGDKODKTIAPTRRSIEVPLMERICLOVSOC     |                                                                          |                                                            |                      |
| STENSEKPSLIVKCIPEPDGDESAVLEOIMHNLSYMKGSVLPERNSPDTNYTL      |                                                                          |                                                            |                      |
| YYMRSLREKHOCENIFREGDSCSDLTIKVDSPFOSVOLMTVDNGKTKRPFNF       |                                                                          |                                                            |                      |
| IYPIITSRYKDDPPRIKTLSTRNDLLTYOMENPAQFIKCLFEYEAVANSOTETHNVYT |                                                                          |                                                            |                      |
| VOEKNENPEPERNEVENTSCPMVGVPDLTLNTLVIRIVKTNKLCEEDKTLMSNSQDEM |                                                                          |                                                            |                      |
| SIGKRNSTLYTMLIVPYVAADAILYLRLKLIIFPPIPDGCKTFEKMEFGILL       |                                                                          |                                                            |                      |
| NDDLHLKKKYDIYKCRTEEDSVALLLENLKASQ"                         |                                                                          |                                                            |                      |
| BASE COUNT                                                 | 477 a                                                                    | 332 c                                                      | 358 g 405 t          |
| ORIGIN                                                     |                                                                          |                                                            |                      |
| Query Match                                                | 36.6%                                                                    | Score 1467.2;                                              | DB 11; length 1572;  |
| Best Local Similarity                                      | 99.1%                                                                    | Pred. No. 0;                                               |                      |
| Matches 1475; Conservative                                 | 0;                                                                       | Mismatches 13;                                             | Indels 0; Gaps 0;    |

[illegible]

| QY         | 1143                                                                                                                                                                                                                                                                                                                                                                                                                             | caagttcttatccctcccaattccgacccgagcaaggtttttaagaagtgttgg          | 1202            |
|------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------|-----------------|
| Db         | 1194                                                                                                                                                                                                                                                                                                                                                                                                                             | CAAGATATATATATCCCTCCCAATTCCTGCATCTCCGCAAGATTTTAAAGAAAGTTTGG     | 1253            |
| QY         | 1203                                                                                                                                                                                                                                                                                                                                                                                                                             | agaccagaatgatatactctgcacctgtaagaagtaagacatctatgagaagcaaccoca    | 1262            |
| Db         | 1254                                                                                                                                                                                                                                                                                                                                                                                                                             | AGACCAGATATGATATACCTGACACTGGAGAAGATAGACATCTATGAGAAAGCAACCA      | 1313            |
| QY         | 1263                                                                                                                                                                                                                                                                                                                                                                                                                             | ggagaacaccacctgagcgtgcgatagaagaacctgaagaacccctcagtatgag         | 1322            |
| Db         | 1314                                                                                                                                                                                                                                                                                                                                                                                                                             | GGAGAAACCGACTCTGTAGTCTGATAGAAACCTGAAGAAACCTCTCAGTATGAG          | 1373            |
| QY         | 1323                                                                                                                                                                                                                                                                                                                                                                                                                             | ataattattttaccctcactgagacctgagacctgaagaattctcccatctccattgta     | 1382            |
| Db         | 1374                                                                                                                                                                                                                                                                                                                                                                                                                             | ATAATTATTTTACCTTCACTGACACTGAGACCTGAGAAAGATCTTCCCATTTTCATTTGTA   | 1433            |
| QY         | 1383                                                                                                                                                                                                                                                                                                                                                                                                                             | tcctgagacctattaaatgtgaaactgaactgaactgaaccattaaacagcgacctcat     | 1442            |
| Db         | 1434                                                                                                                                                                                                                                                                                                                                                                                                                             | TCCTGGAATCTATTATGATGGAACCTGAACCTACTGCGACCAATTTTAAACAGCGACGCTCAT | 1493            |
| QY         | 1443                                                                                                                                                                                                                                                                                                                                                                                                                             | aagagcacacagctcttatgttgatgctgcgcacccgaaacctaanaat               | 1490            |
| Db         | 1494                                                                                                                                                                                                                                                                                                                                                                                                                             | AAGAGCCACAGAGCTTATCTTATGCTGCTAGCGCTAGCAAGACAGAAAGT              | 1541            |
| RESULT     | 6                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                 |                 |
| LOCUS      | S80963                                                                                                                                                                                                                                                                                                                                                                                                                           | 1680 bp                                                         | ROD 27-MAR-1997 |
| DEFINITION | NR4-IL-13 receptor alpha chain [mice, embryonal stem cell,                                                                                                                                                                                                                                                                                                                                                                       |                                                                 |                 |
| ACCESSION  | Genomic/c/mRNA, 1680 nt].                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                 |                 |
| NID        | S80963                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                 |                 |
| VERSION    | 61911503                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                 |                 |
| KEYWORDS   | S80963.1 GI:1911503                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                 |                 |
| SOURCE     | Mus sp. embryonal stem cell.                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                 |                 |
| ORGANISM   | Mus sp.                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                 |                 |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;                                                                                                                                                                                                                                                                                                                                                                    |                                                                 |                 |
| AUTHORS    | Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.                                                                                                                                                                                                                                                                                                                                                                          |                                                                 |                 |
| TITLE      | 1 (bases 1 to 1680)<br>Hilton,D.J., Zhang,J.G., Metcalf,D., Alexander,W.S., Nicola,N.A.<br>Cloning and characterization of a binding subunit of the<br>interleukin 13 receptor that is also a component of the interleukin<br>4 receptor<br>Proc. Natl. Acad. Sci. U.S.A. 93 (1), 497-501 (1996)                                                                                                                                 |                                                                 |                 |
| JOURNAL    | Genbank staff at the National Library of Medicine created this                                                                                                                                                                                                                                                                                                                                                                   |                                                                 |                 |
| MEDLINE    | entry [NCBI gidsb 175604] from the original journal article.                                                                                                                                                                                                                                                                                                                                                                     |                                                                 |                 |
| REMARK     | This sequence comes from Fig. 1.                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                 |                 |
| FEATURES   | Location/Qualifiers                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                 |                 |
| SOURCE     | 1..1680                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                 |                 |
| gene       | /organism="Mus sp."                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                 |                 |
|            | /db_xref="taxon:10095"                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                 |                 |
|            | 61..1335                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                 |                 |
|            | /gene="NR4"                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                 |                 |
|            | /note="IL-13 receptor alpha chain, IL-13 R alpha"                                                                                                                                                                                                                                                                                                                                                                                |                                                                 |                 |
|            | 61..1335                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                 |                 |
|            | /gene="NR4"                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                 |                 |
|            | /note="This sequence comes from Fig. 1; IL-13 R alpha"                                                                                                                                                                                                                                                                                                                                                                           |                                                                 |                 |
|            | /product="IL-13 receptor alpha chain"                                                                                                                                                                                                                                                                                                                                                                                            |                                                                 |                 |
|            | /codon_start=1                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                 |                 |
|            | /protein_id="AA50565.1"                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                 |                 |
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|            | /db_xref="GI:1911504"                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                 |                 |
|            | /translation="MARPALGELILLMTATGVAAATEVOPTPTNSVENC<br>TIITWSPGASPNCTLRYSFELFDQOKIAPENHREELPIDKICQVSOCSA<br>NBEKSEPLKVCISPEGPEASAVMEKCIWNTSYMCSTLPGRTSPDTHITLY<br>WYSLKROCENTVYEGGPHIACSFILTYEBSFEONVOIMKDNAGKIRPCKTYS<br>LTSYVPPDPPIHKLHLKAGALLVOKNRQNFERSCLTYEVENNTQDRIHNTLVEE<br>DKONSEFYTNMGTSIQFLPGVLADAVYTVRVKTNKICEDNKLMSDMSAOSIG<br>KRONSEFYTNMTLTIPVFAVAVITLLFLYKRLKTIIPPIPDGKIFEMFEDQND<br>TLMKKYDIYERKSKETSDVSLNFKKAAP" |                                                                 |                 |
| CDS        | 1..1680                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                 |                 |
|            | 364 C 373 q 432 t                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                 |                 |
| BASE COUNT | 511 a                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                 |                 |



/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
41.880  
/note="IL-13"  
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LCTVITWNPPEASSNCSLMTFSHFQKDKKTAPETRKSTIVPLNERICLQVGSQC  
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YWMRLERKHOCENFEREQYFGCSFDLTKVDSSEFQHSVOIWKDNAGKIKPSEFN  
IVPLTSRVKPDPPHINKLSFHNLDLYWOMENPQNFISRCLEYEVENNSQETHNVEY  
VRF"

BASE COUNT 311 a 231 c 254 g 303 t  
ORIGIN

Query Match 21.5%; Score 862; DB 41; Length 1099;  
Best Local Similarity 100.0%; Pred. No. 8.6e-203;  
Matches 862; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 caacccggcgagctccgagcgagagagctgcatgagctgcccggcgagcttcggagc 61  
DB 9 CAACCCGGCGGCTCCGAGCGCAGAGGCTGCATGAGTGGCCGCGCTCTGCGGGC 68  
QY 62 tctggcgagctgctgctgctgcccggcgagcgagcgagcgagcgagcgagcgagc 121  
DB 69 Tctggcgagctgctgctgctgcccggcgagcgagcgagcgagcgagcgagcgagc 128  
QY 122 aaactaagcagcctgtgacaatttgaagtgctctgttgaacacctgtcacagtaata 181  
DB 129 AAACAGCCACCTGTGACAAATTTGAGTGTCTGTGTTGAAACCTCTGCACAGTATAT 188  
QY 182 ggcagtgaggaatcaccggagggagcgagcctcaattgtatgctatgattagcatt 241  
DB 189 GGCAATGAGATCCACCCGAGGAGCCAGCTCAATTTGATCTATGATTTAGTCATT 248  
QY 242 ttggcgacaacaagaataagaataagctccggaactcgcgttcaatagaatcccc 301  
DB 249 TTGGCGACAACAAGATAAGAAATAGCTCCGAAACTGCTCTTAATGAGAGTACCCC 308  
QY 302 tgaatgaagagatttctcgcgaagtgggtcccaagtgtagcaccacatgagagtgaagc 361  
DB 309 TGAATGAGAGATTCTCTGCAAGTGGGGTCCAGTGTAGCACCAATGAGAGTGAAGC 368  
QY 362 ctggacatttgggttgaataatgcatcaccggaggaagtgaatgctgctgctgctg 421  
DB 369 CTAGCATTTTGGTTGAAAAATGATCTCACCCCAAGAGGTGATCCTGAGTGTGCTGA 428  
QY 422 ctgagctcaatgcatcttggcacaacctgagctacatgaagtgtctctgctccctgga 481  
DB 429 CTGAGCTCAATGCAATTTGGCAACAACCTGAGTACATGAAGTGTCTTGGCTCCGGA 488  
QY 482 ggaatccagctccggcactaactactctactattggcagagagccctggaaaaaa 541  
DB 489 GGAATTCAGGCTCCGACACTACTACTACTACTACTACTACTACTACTACTACTACT 548  
QY 542 ttcataaagtgtaaaacattttagaagagggcaacttgggttcttctttagatcga 601  
DB 549 TTCATCAATGTAAGAAACATCTTAGAGAGGCAATACCTTTGGTGTCTCTTTGATCTGA 608  
QY 602 ccaaaagtgaagattccagtttgaacaacacagtgctccaataatggtccaagataatg 661  
DB 609 CCAAAAGTGAAGATTCCAGTTTGAACAACACAGTGTCCAAATAATGTCAGAGATAAG 668  
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DB 669 CAGGAAAAAATTAACCATCTTCAATATAGTGCCTTTAACTCCCGTGTGAACCACTGATC 728  
QY 722 ctccacataataaaacctctctccacatgagacattatgtgcaatggagaatc 781

DB 729 CTCACATATTAAAAACCTCTCTCCACACATGATGACCTATATGTCATGGGAGATC 788  
QY 782 cacagaatttattagcagatgcctatttataagtagaagtaaacagcacaactg 841  
DB 789 CACAGAAATTTATTACAGATGCTATTTTATGAAGTAAGTCAATACAGCAAACTG 848  
QY 842 agacacataatgcttctacgt 863  
DB 849 AGACAAATATGTTTCTACGT 870

RESULT 8  
LOCUS AF074402 1048 bp mRNA MAN 24-DEC-1998  
DEFINITION Bos taurus interleukin-13 receptor alpha-1 chain precursor, mRNA, partial cds.  
ACCESSION AF074402  
NID 94063012  
VERSION AF074402.1 GI:4063012  
KEYWORDS Bos taurus.  
SOURCE Bos taurus.  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae;  
Bos.  
REFERENCE 1. (bases 1 to 1048)  
Bologna, W.L., Hirano, A., Brown, W.C. and Estes, D.M.  
Biological activities of interleukin-13 on bovine lymphocytes:  
implications for signaling through IL-13R $\alpha$ 1  
Unpublished  
2. (bases 1 to 1048)  
Bologna, W.L. and Estes, D.M.  
Direct Submission  
Submitted (25-JUN-1998) Veterinary Pathobiology, University of  
Missouri-Columbia, W213 Veterinary Medicine Building, Columbia, MO  
65211, USA

## FEATURES

source location/Qualifiers  
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/cell\_type="aortic endothelial"  
CDS  
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/translation="VINLSVSENLCTIITWNPPEGASPNCSLKYSFHKQDKKI  
APLHRSKEVPLNERICLOVGSQCSTNESKPSILVEKCSPPGDESAVTALQCIW  
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WKDNAGKIKPSEFNIVPLTSRVKPDPPHINKLSFHNLDLYWOMENPQNFISRCLEYEV  
ENNSQETHNVEYVRF"

BASE COUNT 321 a 227 c 216 g 284 t  
ORIGIN

Query Match 20.4%; Score 817.6; DB 3; Length 1048;  
Best Local Similarity 86.3%; Pred. No. 8e-192;  
Matches 904; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 136 gtgacaattgagtgctgctggtgaanaacctgcgcagcaagtaataatgagatgaca 195  
DB 1 GTGCAAAATTTGAGTGTCTGTTGAAAACCTGTGCACATCATATGGACATGGAATCCT 60  
QY 196 ccgagggagccagctcaaatgtatgctatgattatgcatcttggcgacaacaa 255  
DB 61 COTGAGGAGCGACAGCCGAATTTGATTAAGTATTCATCTTTTGGCAACAAACAG 120  
QY 256 gataagaataatgctcgggaactcgtcgttcaatagaagtaaccctgaaatgagagatt 315  
DB 121 GATAGAAAATTTGCTCCAGAAATCATCGTTCAAAAGAGTGCCTGTGAACGAGAGATC 180

```

OY 316 tctctcaagtgagggtccagtgtagcaccacagagtgagaagccttagcttgc 375
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DB 181 TGTCTGAGGTGGGTGCCAGTGCAGACAGCAATGAAGTAAAGCCACATTTGGT 240
OY 376 gaaaatgcacccacccacagagtgatcctgagtcctgtgagctgagcttca 435
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DB 241 GAAAGTGTCTTTTCCGCCCTGAGAGTGATCAGAGTCTGTTACTGCGCTCAATGC 300
OY 436 atttgccacacacagtgacagagtgatgctgctgctgctgagagagagagcc 495
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DB 301 ATTGGCACAACCTTAGTATGATGATGATGATGATGATGATGATGATGATGAT 360
OY 496 gac 555
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DB 361 GACCCATACATCTTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 420
OY 556 aac 615
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DB 421 AACTTCTACAGAT 480
OY 616 tccagcttggaagacacacacacacacacacacacacacacacacacacac 675
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DB 481 TCCAGTTTGAACAGACACACACACACACACACACACACACACACACACACAC 540
OY 676 ccatcctcaataatagtgcttcaacttcccggtgaaacacacacacacacac 735
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OY 736 aac 795
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DB 601 AATCTCTCTTCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 660
OY 796 agcagatgctctatcttcaagagagagagagagagagagagagagagagag 855
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DB 661 AGCCAAATGCTTGTGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 720
OY 856 ttctaagtcacag 915
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DB 721 TTTCTAGTTGAAGAGGCCAAATGTCAAGATTTGAAGGAACCTAGAGGATACC 780
OY 916 tcttgcttcaatgagcctggtgcttcttcttcttcttcttcttcttcttct 975
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DB 781 AATTGTTTATGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 840
OY 976 aaaaac 1035
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DB 841 AAAACAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
OY 1036 agtatagtagaag 1095
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DB 901 AGTATAGTACAGAGGCCACATGACATTTTACATTAACCATTTACTCATCTCCAGTC 960
OY 1096 atcgttcagagtgacacacacacacacacacacacacacacacacacacac 1155
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DB 961 ATCGTGTGAGCGCCAGTCAATGCTTCTGCTTATTTGAAGGCTCAAGATCATATA 1020
OY 1156 ttcctcacaatctctgctgctgcaaga 1183
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DB 1021 TTCCCTCCAAATTCCTGATCTGGCAGAGA 1048

```

```

RESULT 9
LOCUS G29644 458 bp DNA STS 05-OCT-1996
DEFINITION human STS SHC-34461, sequence tagged site.
ACCESSION G29644
NID 91593195
VERSION G29644.1 GI:1593195
KEYWORDS STS, STS sequence, primer, sequence tagged site.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

```

# REFERENCE AUTHORS JOURNAL COMMENT

Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 458)  
 Myers, R.M.  
 Unpublished (1996)

Contact: Richard M. Myers  
 Stanford Human Genome Center (SHGC)  
 Stanford University School of Medicine  
 Department of Genetics, M-344, Stanford, CA 94305, USA  
 Tel: 4157259687  
 Fax: 4157259689  
 Email: myers@shgc.stanford.edu

Primer A: TCTGTTATGCTTTGGGGG  
 Primer B: GAATGCTCTCATTTCCCA  
 STS size: 128  
 PCR Profile:

Initial incubation: 94 degrees C for 90 seconds  
 Denaturation: 94 degrees C for 15 seconds  
 Annealing: 62 degrees C for 23 seconds  
 Polymerization: 72 degrees C for 30 seconds  
 PCR Cycles: 30  
 Thermal Cycler: Perkin Elmer 9600

Protocol:  
 Template: 25 ng  
 Primer: each 1 uM  
 dNTPs: each 200 uM  
 Taq Polymerase: 0.05 units/uL  
 Total Vol: 10 uL

Buffer:  
 MgCl2: 2.5 mM  
 KCl: 50 mM  
 Tris-HCl: 20 mM  
 pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from R87164  
 -- Washington University/Merck EST sequence.

## FEATURES

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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /map="x"  
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 primer\_bind 23..42  
 primer\_bind complement(131..150)  
 BASE COUNT 111 a 103 c 110 g 128 t 6 others  
 ORIGIN

Query Match 7.0%; Score 281.8; DB 13; Length 458;  
 Best Local Similarity 96.6%; Pred. No. 1.6e-59;  
 Matches 310; Conservative 0; Mismatches 7; Indels 4; Gaps 2;

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OY 2917 agccac 2976
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DB 6 AGCCAGCCAGCCAGGCTGTTATGCTTTTGGGGGCAATATTTGGTTCATTCTCA 65
OY 2977 cctatccac 3036
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DB 66 CCTATCCACACACATATCGTATATATCCCTCTACTCTTACTTCCCAATTTAAAG 125
OY 3037 aagtatgggaatgagagacattcccccacacacacacacacacacacacacac 3096
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DB 126 AACTATGGGAATAGAGAGCATTTCCCCACCCCATTTCTCTCTACACACAGACTCAT 185
OY 3097 attactggtta-ggaactttagaacttatttccaagttgttcaaatattaccatcata 3155
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DB 186 AATACGTGGTAGGGAACCTTGAACTTATTTCCAAAGTGTTCAAACATTTACCAATCATA 245
OY 3156 ttatataatgagcatttgcacattccctcctagggagggagaga--taagaacc 3212
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\* 9494 10046: contig of 553 bp in length  
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 \* 10047 11400: contig of 1354 bp in length  
 \* gap of unknown length  
 \* 11401 12049: contig of 649 bp in length  
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 \* 12050 12626: contig of 577 bp in length  
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 \* 12627 13518: contig of 892 bp in length  
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 \* 13519 14325: contig of 807 bp in length  
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 \* 14326 15013: contig of 688 bp in length  
 \* gap of unknown length  
 \* 15014 16001: contig of 988 bp in length  
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 \* 16002 16602: contig of 601 bp in length  
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 \* 16603 17537: contig of 935 bp in length  
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 \* 17538 18283: contig of 746 bp in length  
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 \* 18284 18783: contig of 500 bp in length  
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 \* 18784 19778: contig of 995 bp in length  
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 \* 20454 21307: contig of 854 bp in length  
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 \* 21308 22076: contig of 769 bp in length  
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 \* 22077 22743: contig of 667 bp in length  
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 \* 23507 24399: contig of 893 bp in length  
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 \* 27662 27829: contig of 168 bp in length  
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 \* 32586 33411: contig of 826 bp in length  
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 \* 39712 40855: contig of 1144 bp in length

\* 40856 41930: gap of unknown length  
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 \* 49120 50566: gap of unknown length  
 \* contig of 1447 bp in length  
 \* 50567 51600: gap of unknown length  
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 \* 52992 54007: gap of unknown length  
 \* contig of 1016 bp in length  
 \* 54008 55406: gap of unknown length  
 \* contig of 1399 bp in length  
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 \* 56900 59160: gap of unknown length  
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 \* 59161 61384: gap of unknown length  
 \* contig of 2224 bp in length  
 \* 61385 63339: gap of unknown length  
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 \* 66593 67767: gap of unknown length  
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 \* 78870 80157: gap of unknown length  
 \* contig of 1288 bp in length  
 \* 80158 82113: gap of unknown length  
 \* contig of 1956 bp in length  
 \* 82114 84746: gap of unknown length  
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 \* contig of 1720 bp in length  
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 \* contig of 1410 bp in length  
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 \* contig of 1560 bp in length  
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 \* contig of 2154 bp in length  
 \* 91591 93787: gap of unknown length  
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 \* 93788 96557: gap of unknown length  
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 \* 96558 99457: gap of unknown length  
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Query Match 6.3%; Score 253.6; DB 42; Length 141857;  
 Best Local Similarity 84.1%; Pred. No. 4.1e-52;











|   |   |      |                                                                   |      |
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| D | b | 181  | ttggacatggaattccaccgagagagccagctcaaatgttagcttatggaatttttagtcat    | 240  |
| O | y | 241  | tttggcgaacaacaagataagaataatagcttcgggaaactcgtgttccaatagaagtacc     | 300  |
| D | b | 241  | ttttggcgaacaacaagataagaataatagcttcgggaaactcgtgttccaatagaagtacc    | 300  |
| O | y | 301  | ctgaattgagagatttgtctcaagtgggtcccaagtgtgacacaaatgaggttagaag        | 360  |
| D | b | 301  | ctgaattgagagatttgtctcaagtgggtcccaagtgtgacacaaatgaggttagaag        | 360  |
| O | y | 361  | cctagcattttggttgaanaatgcatctcacaccaccaagaagtgaacctgaagtcgtg       | 420  |
| D | b | 361  | cctagcattttggttgaanaatgcatctcacaccaccaagaagtgaacctgaagtcgtg       | 420  |
| O | y | 421  | actgagcttcaatgatatttggcacaaactgagctgaactgaagtgttccttggtccctga     | 480  |
| D | b | 421  | actgagcttcaatgatatttggcacaaactgagctgaactgaagtgttccttggtccctga     | 480  |
| O | y | 481  | aggaataccagtcctcgacactaacatactctcactatgtgacagaagccttgganaaa       | 540  |
| D | b | 481  | aggaataccagtcctcgacactaacatactctcactatgtgacagaagccttgganaaa       | 540  |
| O | y | 541  | attctcaatgtgnaaaacattttaaggaaggccaactttggtgttcccttgatctg          | 600  |
| D | b | 541  | attctcaatgtgnaaaacattttaaggaaggccaactttggtgttcccttgatctg          | 600  |
| O | y | 601  | accaaagtgaaggaattccagcttggacaacacacagctgtgccaataatgtgtcaagataat   | 660  |
| D | b | 601  | accaaagtgaaggaattccagcttggacaacacacagctgtgccaataatgtgtcaagataat   | 660  |
| O | y | 661  | gcaggaataaataaaccactccttaataatagtgtccttaactcccggtgtgaacctgat      | 720  |
| D | b | 661  | gcaggaataaataaaccactccttaataataatagtgtccttaactcccggtgtgaacctgat   | 720  |
| O | y | 721  | cctccacatatnaaaacactccttcacaaatgaatgaactatgtgaatggaggaat          | 780  |
| D | b | 721  | cctccacatatnaaaacactccttcacaaatgaatgaactatgtgaatggaggaat          | 780  |
| O | y | 781  | ccacagaatttbatagcagatgacctatattatgaagtgaagtcaataacagccaact        | 840  |
| D | b | 781  | ccacagaatttbatagcagatgacctatattatgaagtgaagtcaataacagccaact        | 840  |
| O | y | 841  | gagaaacataatgtttcttaagctccaagagagctaaatgtgagaatccagaatttgaaga     | 900  |
| D | b | 841  | gagaaacataatgtttcttaagctccaagagagagctaaatgtgagaatccagaatttgaaga   | 900  |
| O | y | 901  | aatgtggaataacactctgttccatgtgcccgtgtgttccctgataacttgaacaca         | 960  |
| D | b | 901  | aatgtggaataacactctgttccatgtgcccgtgtgttccctgataacttgaacaca         | 960  |
| O | y | 961  | gtccagaataagaatgccaaacaataaagtatatgtctatgaggaatgaacaactctgaagtaat | 1020 |
| D | b | 961  | gtccagaataagaatgccaaacaataaagtatatgtctatgaggaatgaacaactctgaagtaat | 1020 |
| O | y | 1021 | tggagcccaagaatgagatagtgaaagacgaatcccaactctacaataaccatgtta         | 1080 |
| D | b | 1021 | tggagcccaagaatgagatagtgaaagacgaatcccaactctacaataaccatgtta         | 1080 |
| O | y | 1081 | ctcaattgtccagtcacatcgtgcgaagtgaacatagtaactccgttaccctaaanaag       | 1140 |
| D | b | 1081 | ctcaattgtgtccagtcacatcgtgcgaagtgaacatagtaactccgttaccctaaanaag     | 1140 |
| O | y | 1141 | ctcaagattattatattccctcccaactcccgatccctgagcaagaatttttaagaanaatgtt  | 1200 |
| D | b | 1141 | ctcaagattattatattccctcccaactcccgatccctgagcaagaatttttaagaanaatgtt  | 1200 |
| O | y | 1201 | ggaagcccaagaatgatatcactctgacattggaagaagtacacacatctatagaagaacac    | 1260 |
| D | b | 1201 | ggaagcccaagaatgatatcactctgacattggaagaagtacacacatctatagaagaacac    | 1260 |
| O | y | 1261 | aaggaaggaaccgcactctgtatgtcgtgataagaacctgagaagaagcctctcagtgtg      | 1320 |
| D | b | 1261 | aaggaaggaaccgcactctgtatgtcgtgataagaacctgagaagaagcctctcagtgtg      | 1320 |

|    |      |                                                                   |      |
|----|------|-------------------------------------------------------------------|------|
| Dh | 1261 | AAGGAGGAAACCCGACTCTGTGATGTCATGATGAAAGAAACCTGAAGAAAGCCTCTCATGTATGG | 1330 |
| Qy | 1321 | agataattatttttacccttccactctgacacttgagaagattcttccacttccatttgc      | 1380 |
| Df | 1321 | AGATATATTTATTTTACCCTTCACCTGTGACCTTGAGAGATTTCTTCCATTCATTTGT        | 1380 |
| Qy | 1381 | tatctgggaactcttaatactgaaactgaaactacgcaccatttaaaagaagcagctc        | 1440 |
| Dh | 1381 | TATCTGGGAACCTTTTAAATGGAAGCTGAAGACTGTGACCATTTTAAAGCAGGAGTCC        | 1440 |
| Qy | 1441 | ataagcgccacaagctcttattgtgtagtcgcgacccgaaataataatgvgcgtc           | 1500 |
| Dh | 1441 | ATAAGAGCCACAGGCTCTTATGTTGATGTCGCACCGAAGAAAACATAATATGCGGCT         | 1500 |
| Qy | 1501 | ttgggaagagtgctggagctatccatcgaatttaaaagccagcagcttcaactag           | 1560 |
| Dh | 1501 | TTGGGAAGAGTGTGAGCATCTTCTCATGTATATATAAGCAGCAGCTTCAACTAG            | 1560 |
| Qy | 1561 | gggacaagaacaagaatgatgatagatggtggagttaatcttaacaaggttgacaact        | 1620 |
| Dh | 1561 | GGGACAAGCAAAAAGATAGATAGTGGAGTTATCTTATCAAGAGTTGTACAACAT            | 1620 |
| Qy | 1621 | tcttgaggatctatcttcttcttggttccttggtcaacttgacaacttaattattgt         | 1680 |
| Dh | 1621 | TCTTGAGGAGATCTATCTTCTTGTGTTGTTGTCAACTGACATAAATTTATTTGT            | 1680 |
| Qy | 1681 | aggggaaactctttgggggtgcaaatgctaagtccaacttgatcacaaagaacatgtag       | 1740 |
| Dh | 1681 | AGGGAACTCATTTGGGGGTCAAAATGCTAATGCAAACTTGAGTCACAAAGACATGTAG        | 1740 |
| Qy | 1741 | aaaacaataatgataaaactctgatatgtattgtttggagatcctatitgacaatgtttgtg    | 1800 |
| Dh | 1741 | AAAAAAAATGATAAAATGTGATATGATTTTGGATGCTATATGAAACATGTTGTG            | 1800 |
| Qy | 1801 | gctatataactctttaacagctctgagcttggtccggctggcagcgttaatccag           | 1860 |
| Dh | 1801 | GCTATTAAACTCTTTTAACAGCTGTGGCTGGGTCCGGTGCATCGCTTAATCCAG            | 1860 |
| Qy | 1861 | caatttggagtcctcgagcgggcgagatcacctcgaggttcagagatccagacagctgac      | 1920 |
| Dh | 1861 | CAATTTGGGAGTCCGAGCGGCGGAGATCACTGAGGTCCAGAGTCCAGACACCTGAC          | 1920 |
| Qy | 1921 | caaaatggtagaacctctctcttcaaaaaaacataaaatnaactagggtgtggtggcg        | 1980 |
| Dh | 1921 | CAAAATGGTAGAACCTCTCTCTCTACTTAACATAACAAAATTAACGTGGGTGTGGTGGCG      | 1980 |
| Qy | 1981 | tgcctgtaatcccgactcctcggaagcctgagcagctgaaattgtttbaactctggagct      | 2040 |
| Dh | 1981 | TGCCGTGTAATCCAGCTACTCTGGGAAGCTGAGGCAAGTGTAATGTTGAACCTGGAGGT       | 2040 |
| Qy | 2041 | ggaggttgtagtgagcagagatacaacacacctgcaactctagcctgggtgtacagagcaaac   | 2100 |
| Dh | 2041 | GGAGGTTGCACTGAGCAGAGATATACACCACTGCACTTAAGCTGGGTGTACAGACAAGAC      | 2100 |
| Qy | 2101 | tctctcctcaaaaaacaacaacaacaacaacaacaacaacacctttaatttctggagt        | 2160 |
| Dh | 2101 | TCTCTCTAAAAACAACAACAACAACAACAACAACAACAACAACCTTTATTTTGGAGT         | 2160 |
| Qy | 2161 | catcatctcctctcgacagcatcttctctctgtcttgaagcccccagaatactagtgctgc     | 2220 |
| Dh | 2161 | CATCATCTCCCTTCACAGCACTTTTCTCTGCTTTGAAGCCCAAGAAATCAGTGTGGCC        | 2220 |
| Qy | 2221 | atgtatgacaactacaagaanaacacagagggaagcttctttgccaagaacctttaagccatt   | 2280 |
| Dh | 2221 | ATGTATGACAACCTATACGAAAAACACAGGAGGAGCTTTTGGCCAAGACCTTTCAAGGCATT    | 2280 |
| Qy | 2281 | tttagcctgttaaggcagctgagtgaaatgacatcctctgggttatatagaatctcaacatg    | 2340 |
| Dh | 2281 | TTTAGCTGTTAGGGCAGCTGAGAGTGAATGATGCTCTTGGGATTAAGAGTTCAACATG        | 2340 |
| Qy | 2341 | aagctctcaacatgtaatttcttcaactctgtactccaagttagcatttactgtgtctt       | 2400 |
| Dh | 2341 | AAGCTCTAACAAATGTTTTCTTCACTCTCTCTCACTCAAGTAGCAATTAATGTGTCTT        | 2400 |

|    |      |                                                                  |      |
|----|------|------------------------------------------------------------------|------|
| QY | 2401 | ggttggtgtaagccccggggtgtgaagcaacagacccttcagggggttaacgctatt        | 2460 |
| Db | 2401 | gggttgggtgaagccccccggggtgtgaagcaacaccccttcagggggttaacgctatt      | 2460 |
| QY | 2461 | tgaagctccctcagttctcttgccactttttttttaaactccaccagtcattttcagacct    | 2520 |
| Db | 2461 | tgagactcctcagttctcttgccactttttttttaaactccaccagtcattttcagacct     | 2520 |
| QY | 2521 | tttaactcctcaattcccaacactgattccccccttttgcaattccctctccctccctc      | 2580 |
| Db | 2521 | tttTAACtCCTCAATTCACAACACAGATTTCCCTTTTGCAATTCCTCTCCCTTCCTT        | 2580 |
| QY | 2581 | gtagaccttgactcttcatttggaataatgaatgataatcgcctcagaagagacccgaagag   | 2640 |
| Db | 2581 | GTAGCCCTTTGACTTTTCATTGGAAATTAAGATTAATATCGCTCAGAGACACTGAGAGAG     | 2640 |
| QY | 2641 | caggagataattagcaatcctcaggttaagtgtgagtaactcagaaacaatgactaattct    | 2700 |
| Db | 2641 | CAGAGAGATTAATAGCATCTCAGGTTTAACTGTGATCGATATCGAATAACAAAGACTAATCT   | 2700 |
| QY | 2701 | tgcatatttggaaactccatgctggaaggttttcagatgataattgttgattttccaaa      | 2760 |
| Db | 2701 | tgCATATTtTgAACTCCATGtGAGGgtTtTtAGAtTGAATtTtGTGCAATtTTCAAA        | 2760 |
| QY | 2761 | cagagatgaagtgtgattcttcacgtlaagaaacttgattgcctctgaagaaanaaagaatag  | 2820 |
| Db | 2761 | CAGAGATGAGGtGTATCTTCACGTGAACAATGTGATTCGTGAGAAAAAAGAAATAG         | 2820 |
| QY | 2821 | ttgaaacctattcctctcttctttaaagaatgggtgcagaagatcctctcttctctgcataa   | 2880 |
| Db | 2821 | TTGAACCTAATTTCTCTTTCTTTAACAAAGATGGGtCCAGAGATTCCTCTTTCTCTGCCATAA  | 2880 |
| QY | 2881 | atgattaataatagctcttgctgtcttacaattggttagccagccagccaaagctctgtt     | 2940 |
| Db | 2881 | ATGATTAAATTAATATAGCTTTTGTGTCTTACATTGGTATGACGACGCAAGGCTGTCTT      | 2940 |
| QY | 2941 | atgcttttggggggacalatatattgggttccattctcaacttcacacaacacatccglat    | 3000 |
| Db | 2941 | ATGCTTTTtGGGGGtCAATATtGGGtTTCATTCtCACTTCACATTCACACAAACATATCCGTAT | 3000 |
| QY | 3001 | atatcccccctcactcttacttcccccaatttaagaagaatgaggaatgaagggacctt      | 3060 |
| Db | 3001 | ATATCCCTCTACTCTTACTCTCCCTCAAAATTAAGAAGATGGGAATATAGAGGCAATTT      | 3060 |
| QY | 3061 | cccccaaccccaattctctctccacacacagactcatalactgtgtgaagacttgaagact    | 3120 |
| Db | 3061 | CCCCAACCCCAATTTCTCTCTCTACACACAGACTCATATTATCTGTGAGAACTTGAGAACT    | 3120 |
| QY | 3121 | ttatttccaaagtgtgtcaaacatttaccacatacataataacaatgatagtctattgcaat   | 3180 |
| Db | 3121 | TTATTTCCAAGTGTTCACAACATTTNACCAATCATATTAAATACATGATGCTATTTCGAAT    | 3180 |
| QY | 3181 | tccctgcctccaaaggagagataaagaacccctcaactcctcaagtttgggttaacagt      | 3240 |
| Db | 3181 | TCCTCTCTCTAAGGAGGGGAGATATAGAACCCTCACTCTCTACAGGTTTGGGTACAACT      | 3240 |
| QY | 3241 | ggcaacactgcttcacatgycggtgtagaagcaatggtgcctgctctctcgaagaagctg     | 3300 |
| Db | 3241 | GGCAACCTGCTTCACATGCGCGGTATGAACATAGTGCCCTGCTCTCTGAGGAAGCTGG       | 3300 |
| QY | 3301 | ggttcaatagaatagcaatgtfaaaattttcttgaagtaagaattgaagcttgggaagcag    | 3360 |
| Db | 3301 | GGTTATATGCAATGGCAGATGTAAATTTATCTTGAAGTCAAGTTGAGGCTGGGAGACAG      | 3360 |
| QY | 3361 | ccgtatgaatglttctactttgttctcgcgtttctcagaagaagataattggtttccgt      | 3420 |
| Db | 3361 | CCGTATGATGATGTCTACTTTGTCTGTCTGTCTAGAAAGAAATTTTGGTTTCTGT          | 3420 |
| QY | 3421 | atagaagaatgaagtaattctcttccagatatttataattctgggaagcaaaacccatgc     | 3480 |
| Db | 3421 | ATAGAAGATGAGTAAATTCCTCTTCAGGATTTTATTAATTTCTGGGAAGCAAAACCCATGC    | 3480 |

|        |                                                                     |                                                                 |      |
|--------|---------------------------------------------------------------------|-----------------------------------------------------------------|------|
| CY     | 3461                                                                | ctcccccbaagcatttttactgtatcacccatttagatgacgcataagaaggatgcttgaa   | 3540 |
| DZ     | 3491                                                                | ctccccctaccacattttttactgttatcttaatttaaagccattgaagggatgcttgaa    | 3540 |
| OI     | 3511                                                                | atcccacaacaacattgatgacttacagtcatactcaagtctctggagatgggaatgaccttt | 3600 |
| Fb     | 3541                                                                | ATTGCCAACAACACTTGATGAGCTGACAGTGTACGTGGGAGTGGGAAGTAGATCTTTT      | 3600 |
| CJ     | 3601                                                                | gttccactcctctcttttttagcagtaaaaatagctcgagggaagaaagggaagaaagagt   | 3660 |
| Lb     | 3601                                                                | GTTCCCACTCCTCTTCCTTTTAGCAGTAAATPACTGAGGGAAGGAGGAAAAAGAAGAGT     | 3660 |
| OY     | 3661                                                                | tatggagatccctggtggtggtgtgtatgccctgactgcttggagagccttgagagtgctat  | 3720 |
| Df     | 3661                                                                | TATGGGAATACCCTGTGGTGGTGTGTATGCCCTAGCGCTTGGGAGCTTGGAGGTGTCTGT    | 3720 |
| CY     | 3721                                                                | atcagtgatattcccatccctctggtggaatatagtaggctcatctactctttagtgctca   | 3780 |
| Nb     | 3721                                                                | ATCAGTGATATTCOCATCCCCTGTGGGAATTAAGTAGGCCTATTACGTTTAGTGCTA       | 3780 |
| CY     | 3781                                                                | gccaatgtgatttttctcctaatacctaagaacaaccaglytcaagatgtaattcct       | 3840 |
| Eh     | 3781                                                                | GCCATATGATTTTTTTCCTAACATACCTAACAACCAACCCAGTGCAGATGTAATCTT       | 3840 |
| OY     | 3841                                                                | attctcttctgtcagtaaatgttttccctcactcctggtgacatgagggatagtaaacaa    | 3900 |
| Dd     | 3841                                                                | ATTCTTTCGTACGATTAAGTTTTCCTTCATCATCTGGGCACTGAAGGATATGTAAACAA     | 3900 |
| OY     | 3901                                                                | tgtaacatttttgtgtagcttcaaccaaggagatgttctctttaactctctatagaa       | 3960 |
| Dj     | 3901                                                                | TGTTAATTTTGTGTAGCTTCAACCAAGGATTTTCTGTGTTAACCTCTTAAGGAAA         | 3960 |
| OY     | 3961                                                                | gtcttgagtaaaaaatattgtctcttttgtatgtacccaacaaaaaa 4009            |      |
| Ed     | 3961                                                                | GCTTGATTAATAATTAATATGTCTTTTGTATGTCACCAAAAAAAAA 4009             |      |
| RES37T | 2                                                                   |                                                                 |      |
| ID     | T66165                                                              | standard; DNA; 1383 BP.                                         |      |
| AC     | T66165;                                                             |                                                                 |      |
| DE     | 15-JUN-1997                                                         | (first entry)                                                   |      |
| DE     | Human Interleukin-12 receptor alpha chain NR4 DNA.                  |                                                                 |      |
| KM     | NR4; haemopoietin receptor; Interleukin-13 receptor; IL-13;         |                                                                 |      |
| KW     | Cytokine; allergy; asthma; therapy; ss.                             |                                                                 |      |
| OS     | Homo sapiens.                                                       |                                                                 |      |
| FH     | Key                                                                 | Location/Qualifiers                                             |      |
| FT     | cds                                                                 | 61..1341                                                        |      |
| FT     |                                                                     | /+tag-a                                                         |      |
| FT     | signal_peptide                                                      | 61..141                                                         |      |
| FT     |                                                                     | /+tag-b                                                         |      |
| FT     | mcd_peptide                                                         | 142..1338                                                       |      |
| FT     |                                                                     | /+tag-c                                                         |      |
| PN     | R09735663-A1.                                                       |                                                                 |      |
| PD     | 01-MAY-1997.                                                        |                                                                 |      |
| PF     | 23-OCT-1996; A00668.                                                |                                                                 |      |
| PE     | 23-OCT-1995; AU-006135.                                             |                                                                 |      |
| Pk     | 22-DIC-1995; AU-007276.                                             |                                                                 |      |
| Pz     | 09-SEP-1996; AU-002208.                                             |                                                                 |      |
| EA     | (AMRA-) AMRAD OPERATIONS PVT LTD.                                   |                                                                 |      |
| FJ     | Hilton DJ, Mercalf D, Nicola NA, Willson T, Zhang JG;               |                                                                 |      |
| DR     | WPI; 97-259018/73.                                                  |                                                                 |      |
| EL     | J-PDB: M09822.                                                      |                                                                 |      |
| PT     | DNA encoding animal haemopoietin receptor which interacts with      |                                                                 |      |
| PT     | interleukin-13 useful to treat asthma, allergy or condition         |                                                                 |      |
| PT     | exacerbated by IGE production                                       |                                                                 |      |
| PS     | Claim 6; Page 52-54; 93pp: English.                                 |                                                                 |      |
| CC     | DNA sequences (T66164 and T66165) respectively code for novel mouse |                                                                 |      |
| CC     | and human haemopoietin receptors (M09821 and M09822) designated NR4 |                                                                 |      |
| CC     | that comprise the interleukin-13 (IL-13) receptor alpha-chain. A    |                                                                 |      |
| Cc     | human bone marrow cDNA library was screened with probes comprising  |                                                                 |      |
| CC     | nucleotides 82-840 and 840-1270 of murine NR4 cDNA, and a composite |                                                                 |      |
| CC     | sequence for human NR4 was produced from isolated clones. The       |                                                                 |      |

1

[illegible]

|    |      |                                                                    |      |
|----|------|--------------------------------------------------------------------|------|
| QY | 907  | gagaatcatctgtttcttcattgctccctcgtcgtgtctctccgtaactcttgaaacagtcaga   | 966  |
| Db | 931  | GAGAAATACCTCTTTTTCATGAGTCCCGGTGTCTCTCGTACTTTGAAACAGTCCAGA          | 990  |
| QY | 967  | ataagagtcacaaacaataagttatctatctgtgagatgacaaactctgtagtaattgagc      | 1026 |
| Db | 991  | ATAAGAGTCAAAACAAATAAGTATCTCTATGAGATGACAAACTCTGGAGTAATTGGAGC        | 1098 |
| QY | 1027 | caaaaatgagttatagttagaagacgcgaattccacactcaataacatgttactatt          | 1088 |
| Db | 1051 | CAAAATATGATTTAGTATGAGTAAGAGGCATTCACACTCTACATACCATGTTTACTATT        | 1111 |
| QY | 1087 | gttccagtcattcgtcgaagtgacatctagttactcctgcttaccctaaagaagctcaag       | 1144 |
| Db | 1111 | GTTCCAGTCACTGTCGACAGTGCATCATTAATCTCTCTGCTTAACTTAAAGAAAGCTCAAG      | 1177 |
| QY | 1147 | attatattatcccccacaattccctcgatctctgycacaagatttttaagaagaatgtttgagac  | 1200 |
| Db | 1171 | ATTATTATATTCCTCCCAATTCCTCGAATCCGAGACCTGGCAAGATTTTAAAGAAATGTTTGAGAC | 1233 |
| QY | 1207 | cgaagtgtatgactctgcactctgtaagaagaatagacatctctatgaaagaacaaacgaagag   | 1266 |
| Db | 1231 | CAGATGTATGATCTCTGCATCTGCACTGSAAMAATACGACATCTATGAGAAAGCAAACTCAAGAG  | 1299 |
| QY | 1267 | gaaccgcactctgtagtcgtcgtatagaanaacctgaaagaagcctctcgaatgagtagagataa  | 1328 |
| Db | 1291 | GAAACGACTCTGTAGTGTGATGAGATGAAAACCTGAAAGAAAGCTCTACGATGATGAGATTA     | 1350 |
| QY | 1327 | tttatcttaacctcaactcgtgacctcggagaaga                                | 1359 |
| Db | 1351 | TTTTATTTTACTTCACTGAGACTCTGGAATAA                                   | 1383 |

|         |                                                                     |
|---------|---------------------------------------------------------------------|
| RESULT  | 3                                                                   |
| T66164  |                                                                     |
| ID      | T66164 standard; DNA; 1383 BP.                                      |
| AC      | T66164                                                              |
| DT      | 15-JUL-1997 (first entry)                                           |
| DE      | Mouse interleukin-12 receptor alpha chain NR4 DNA.                  |
| KW      | NR; haemopoietin receptor; interleukin-13 receptor; IL-13;          |
| OS      | cytokine; allergy; asthma; therapy; ss.                             |
| Mus sp. |                                                                     |
| Key     |                                                                     |
| FF      | Location/Qualifiers                                                 |
| FF      | cds                                                                 |
| FF      | 61..1341                                                            |
| FF      | /tag= a                                                             |
| FF      | 61..141                                                             |
| FF      | /tag= b                                                             |
| FF      | mat_peptide 142..1338                                               |
| FF      | /tag= c                                                             |
| FF      | musc_difference 121..123                                            |
| FF      | /tag= d                                                             |
| FF      | /note="bases 121-123 (nm) code for an unidentified amino acid"      |
| FF      | 640..642                                                            |
| FF      | /tag= e                                                             |
| FF      | /note="bases 640-642 (nm) code for an unidentified amino acid"      |
| PV      | WO9715663-A1.                                                       |
| PI      | 01-MAY-1997.                                                        |
| PR      | 23-OCT-1996; AU0668.                                                |
| PK      | 23-OCT-1995; AU-006135.                                             |
| PR      | 22-DEC-1995; AU-007276.                                             |
| PA      | 09-SEP-1996; AU-002208.                                             |
| PR      | (AMLA-) AMRAD OPERATIONS PTY LTD.                                   |
| PI      | Hilton DJ, Mercat D, Nicola NA, Willson T, Zhang JG;                |
| DE      | Wpi; 97-239018/23.                                                  |
| DE      | P-FSDS; W09821.                                                     |
| PT      | DNA encoding animal haemopoietin receptor which interacts with      |
| PT      | interleukin-13 - useful to treat asthma, allergy or condition       |
| PS      | exacerbated by ICE production                                       |
| CC      | Claim 6; Page 48-50; 93pp; English.                                 |
| CC      | DNA sequences (T66164 and T66165) respectively code for novel mouse |
| CC      | and human haemoprotein receptors (W09821 and W09822) designated NR4 |



as immune stimulants or suppressors, e.g. for viral, bacterial or fungal infections, for autoimmune diseases such as multiple sclerosis or systemic lupus erythematosus, to regulate haematopoiesis, for tissue growth, as an activator or inhibitor, or as a chemotactic or chemokinetic, haemostatic and thrombolytic, receptor/ligand, or anti-inflammatory or tumour inhibitor agents.

Sequence 592 BP; 197 A; 121 C; 105 G; 169 T;

Query Match 14.8%; Score 592; DB 1; Length 592;  
Best Local Similarity 100.0%; Pred. No. 1.3e-136;  
Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 585 ttgttccttgatctgacccaagtgaagatccagtttgtaacaacagtcgccaat 644  
DB 1 ttgttccttgatctgacccaagtgaagatccagtttgtaacaacagtcgccaat 60  
QY 645 aatgtaagaataatgaggaataaataacatcccttaataatagtccttaattc 704  
DB 61 AATGCTCAAGATATGAGGAAAAATTAACCATCCCTCAATATAGTGCCTTAATCTC 120  
QY 705 ccgtgtgaacatctgacccacataataaaccctctccctcaaatatgacctata 764  
DB 121 CCGGTGAACCTGATCCTCCACATATTAACCTCTCTCCACATATGAGCTATA 180  
QY 765 ttgtcaatgagagatccacagaatttattagacagatgacctattatgaagtaga 824  
DB 181 TGTCGAATGGAGATCCACAGATTTTATGACAGATGCCCTATTTATGAGTAGAGT 240  
QY 825 caataacagcaaacctgagacacataatgtttctgacgaagagctaaatgtagaa 884  
DB 241 CAATTAACGACCAACTGAGACACATATGTTTCTACGTCCAAAGGCTTAAAGTAGAA 300  
QY 885 tccagaattgagagaatgtagaatacatctgtttcaatggtccgtgtctcc 944  
DB 301 TCCGAATTTGAGAGAAATGTGAGATACATCTGTTTCATGTCCTGCTGTTCTTC 360  
QY 945 tgaacttgaacacagtcagcaataagagtcacaaacaataagttatgctagaagata 1004  
DB 361 TGATACTTTGAACACAGTCGATGATTAAGAGTCACAAACAAATAGTATGAGAGATGA 420  
QY 1005 caaaccttgagtaattgtagcagaanaatgtagatagtagaagcgcgaattccacact 1064  
DB 421 CAAACCTGTGAGTAATTTGAGCCCAAGAAATGAGTATAGTAAGAGCCGAATTCACACT 480  
QY 1065 ctacataacatgtaattctatgttccagtcacatgtagcaggtgcaatcattgacctc 1124  
DB 481 CTACATTAACCATGTTACTATGTTCCAGTCATCGTCGAGGTGCAATCATAGTACTCCT 540  
QY 1125 gcttaactaaaggctcaagattatattatccctcaattcctgacct 1176  
DB 541 GCTTACCTAAAAAGCTCAAGATTATATATTCCTCCCAATTCCTGATCCT 592

## RESULT 5

V89658  
ID V89658 standard; cDNA; 391 BP.  
AC V89658;  
DT 15-FEB-1999 (first entry)  
DE EST clone DA136.  
KW Human; secreted protein; expressed sequence tag; EST; haematopoiesis;  
KW tissue growth; activin; inhibitor; chemotaxis; chemokinetic; haemostatic;  
KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;  
KW gene therapy; ss.  
OS Homo sapiens.  
PN WO9845436-A2.  
PD 15-OCT-1998.  
PF 10-APR-1998; US-6955.  
PR 10-APR-1997; US-838821.  
PA (GENE) GENETICS INST INC.  
PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D,  
PI Racie LA, Spaulding V, Treacy M;  
PI WPI; 99-07007/06.

PT New polynucleotides encoding human secreted proteins - derived from  
PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,  
PT ovary, pituitary, retina and colon cDNA libraries.  
PS Claim 1: Page 288, 618pp; English.

CC The present sequence represents a human expressed sequence tag (EST).  
CC The polynucleotide, which is a secreted EST, and the encoded protein  
CC are predicted to have useful biological activities which would make  
CC them suitable for treating, preventing or ameliorating medical  
CC conditions in humans and animals, although no supporting data is  
CC given. Suggested activities include nutritional activity, immune  
CC stimulating or suppressing activity, haematopoiesis regulating  
CC activity, tissue growth activity, activin/inhibin activity,  
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic  
CC activity, receptor/ligand activity, anti-inflammatory activity,  
CC cadherin/tumour invasion suppressor activity, tumour inhibition  
CC activity. The polynucleotide may also be useful for gene therapy.

Sequence 391 BP; 127 A; 82 C; 75 G; 107 T;

Query Match 9.0%; Score 360.8; DB 1; Length 391;  
Best Local Similarity 99.5%; Pred. No. 9.8e-80;  
Matches 362; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 824 tcaataacagcaaacctgagacacataatgtttctgacgaagagctaaatgtaga 883  
DB 24 TCATATACGCCAACTGAGACACATATGTTTCTACGTCCAAAGGCTTAAAGTAGAGA 83  
QY 884 atccagaattgagagaatgtagaatacatctgtttcaatggtccgtgtctcc 943  
DB 84 ATCCGAAATTTGAGAGAAATGTGAGATACATCTGTTTCATGTCCTGCTGTTCTTC 143  
QY 944 ctgatacttgaacacagtcagcaataagagtcacaaacaataagttatgctagaagatg 1003  
DB 144 CTGATCTTTGAACACAGTCGATGATTAAGAGTCACAAACAAATAGTATGCTATGAGAGT 203  
QY 1004 acaaaccttgagtaattgtagcagaanaatgtagatagtagaagcgcgaattccacac 1063  
DB 204 ACAACCTGTGAGTAATTTGAGCCCAAGAAATGAGTATAGTAAGAGCCGAATTCACACT 263  
QY 1064 tctacataacatgtaattctatgttccagtcacatgtagcaggtgcaatcattgacctc 1123  
DB 264 CTACATTAACCATGTTACTATGTTCCAGTCATCGTCGAGGTGCAATCATAGTACTCCT 323  
QY 1124 tgccttaactaaaggctcaagattatattatccctcaattcctgacctgagaga 1183  
DB 324 TGCTTACCTAAAAAGGCTCAAGATTATATATTCCTCCCAATTCCTGATCCTGCCAAGA 383  
QY 1184 tttt 1187  
DB 384 ATCT 387

## RESULT 6

V11621  
ID V11621 standard; cDNA; 340 BP.  
AC V11621;  
DT 11-SEP-1998 (first entry)  
DE Homo sapiens adult placenta clone DA136.11 5' region.  
KW adult; placenta; cDNA library; clone DA136.11; anti-inflammatory;  
KW therapeutic composition; autoimmune disease; immune; stimulation;  
KW suppression; ds.  
OS Homo sapiens.  
PN WO9814576-A2.  
PD 09-APR-1998.  
PF 03-OCT-1997; U18007.  
PR 04-OCT-1996; US-726237.  
PA (GENE) GENETICS INST INC.  
PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D,  
PI Racie LA, Spaulding V, Treacy M;  
PI WPI; 98-240082/21.  
PI Nucleic acids encoding novel secreted proteins - useful as, e.g.  
PI anti-inflammatory, immuno-stimulatory or suppressing agents  
PI Claim 45; Page 80; 110pp; English.



CC The sequence is that of an isolated polynucleotide which may  
 CC be of use in the production of therapeutic compositions for  
 CC treating or ameliorating a medical condition in a mammal. Such  
 CC compositions may be used for, e.g. research purposes as markers for  
 CC tissues, molecular weight markers for gels, primers or probes, for  
 CC nutrition as carbon, nitrogen or carbohydrate source. They can also be  
 CC used as a cytokine for cell proliferation and differentiation activity,  
 CC as immune stimulants or suppressors, e.g. for viral, bacterial or fungal  
 CC infections, for autoimmune diseases such as multiple sclerosis or  
 CC systemic lupus erythematosus, to regulate haematopoiesis, for tissue  
 CC growth, as an activator or inhibitor, or as a chemotactic or  
 CC chemokinetic, haemostatic and thrombocytic, receptor/ligand,  
 CC anti-inflammatory or tumour inhibitor agents.  
 SO Sequence 340 BP; 101 A; 73 C; 79 G; 85 T;

Query Match 8.4%; Score 336.4; DB 1; Length 340;  
 Best Local Similarity 99.1%; Pred. No. 9.4e-74;  
 Matches 337; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 120 ggaactcagccacctgtacaaattgtctctgttgaanaactctgcacgaatt 179  
 DB 1 GGAAGCTCACCACCTGTACAAATTGAGTCTCTGTGAAACCTGCAAGTAAT 60  
 OY 180 atgacatgaaatccaccagagagagagagagagagagagagagagagagag 239  
 DB 61 ATGACATGAGATCCACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120  
 OY 240 ttctggcgaacaaagaagaagaagaagaagaagaagaagaagaagaagaaga 299  
 DB 121 TTTTGGCGCAACAAGATAGAAATAGCTCCGAAATCGCTGTAATAGAAATAC 180  
 OY 300 cctgaatagagagattgtctcaagtgggtccagctgtagacaaatgagaaga 359  
 DB 181 CCGATGAGAGAGATTGTCTGCAAGTGGGTCACAGGTATACCAAGAGAGTAGAA 240  
 OY 360 gctcagcatttggttgaaatgcatctcaccaccagagagagagagagagag 419  
 DB 241 GCTTGCATTTGGTTGAAATAATGATCTCACCCAGAGAGATCGTAATCTCTGT 300  
 OY 420 gactgaagctcaatgacatttgcacaaactgagctacatg 459  
 DB 301 GACTGAGCTTCAATGATTTGGCACAACTGAGCTACATG 340

## RESULT 7

V11623 standard; cDNA; 285 BP.  
 ID V11623  
 AC V11623;  
 DT 11-SEP-1998 (first entry)  
 DE Homo sapiens adult placenta clone DA136.11 3' region.  
 KW adult; placenta; cDNA library; clone DA136.11; anti-inflammatory;  
 KW therapeutic composition; autoimmune disease; immune; stimulation;  
 KW suppression; ds.  
 OS Homo sapiens.  
 KM WO9814576-A2.  
 PN 09-APR-1998.  
 PD 03-OCT-1997.  
 PR 04-OCT-1996; US-726237.  
 PA (GENY) GENETICS INST INC.  
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Werberg D,  
 PI Racine LA, Spaulding V, Treacy M;  
 DR WPI: 98-240082/21.  
 PT Nucleic acids encoding novel secreted proteins - useful as, e.g.  
 PT anti-inflammatory, immuno-stimulatory or suppressing agents  
 PS Claim 45; Page 82; 110p; English.  
 CC The sequence is that of an isolated polynucleotide which may  
 CC be of use in the production of therapeutic compositions for  
 CC treating or ameliorating a medical condition in a mammal. Such  
 CC compositions may be used for, e.g. research purposes as markers for  
 CC tissues, molecular weight markers for gels, primers or probes, for  
 CC nutrition as carbon, nitrogen or carbohydrate source. They can also be  
 CC used as a cytokine for cell proliferation and differentiation activity,

CC as immune stimulants or suppressors, e.g. for viral, bacterial or fungal  
 CC infections, for autoimmune diseases such as multiple sclerosis or  
 CC systemic lupus erythematosus, to regulate haematopoiesis, for tissue  
 CC growth, as an activator or inhibitor, or as a chemotactic or  
 CC chemokinetic, haemostatic and thrombocytic, receptor/ligand,  
 CC anti-inflammatory or tumour inhibitor agents.  
 SO Sequence 285 BP; 93 A; 36 C; 50 G; 98 T;

Query Match 6.4%; Score 258.4; DB 1; Length 285;  
 Best Local Similarity 96.6%; Pred. No. 1.4e-54;  
 Matches 259; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 3742 tctgggaattagtagccattactgttttaggtcagcagctgtgattttcccta 3801  
 DB 1 TGTGGAAATTAATAGGCTCATTTACTGTTTAGGCTGACNATATGATTTTCTTA 60  
 OY 3802 acatacctaagcaaacacagctgacagatgtaattcttattcttcgtcagtaagt 3861  
 DB 61 ACATCTTAAGCAACCCAGNGTCAGATGAGNATNTTATTTCTTCGTTCACTTAAGTT 120  
 OY 3862 ttccctcattcagcagcagcagcagcagcagcagcagcagcagcagcagc 3921  
 DB 121 TTTCCATTATNNGGCGCACTGAAGGATATGTAAACAATGTTTACATTTTGTGTT 180  
 OY 3922 tcaacagagatgttctctgttacttctttagaagaagcttgagtaataatattg 3981  
 DB 181 TCACCCGAGATTTGTTCTGTTTAATCTTTATAGAAACCTTGATTAATAATATTG 240  
 OY 3982 tcttttgcattgcaccccaaaaaa 4039  
 DB 241 TCTTTTGTATGTCACCAAAAAA 268

## RESULT 8

T22947  
 ID T22947 standard; cDNA to mRNA; 265 BP.  
 AC T22947;  
 DT 24-OCT-1996 (first entry)  
 DE Human gene signature HUMGS04672.  
 KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;  
 KW human; cloning; mapping; non-biased library; diagnosis; detection;  
 KW cell typing; abnormal cell function; ss.  
 OS Homo sapiens.  
 PN WO9514772-A1.  
 PD 01-JUN-1995.  
 PF 11-NOV-1994; J01916.  
 PR 13-NOV-1993; JP-355504.  
 PA (MATSU) MATSUBARA K.  
 PA (OKUBO) OKUBO K.  
 PI Matsubara K, Okubo K;  
 DR WPI: 95-206931/27.  
 PT Identifying gene signatures in 3'-directed human cDNA library - e.g.  
 PT for diagnosis of abnormal cell function, by preparing cDNA that  
 PT reflects relative abundance of corresp. mRNA in specific human  
 PT tissues  
 PS Claim 1; Page 1252; 2245pp; Japanese.  
 CC A single-stranded DNA (or its complementary strand or the corresp.  
 CC double-stranded DNA) which comprises one of the 7837 "GS" sequences  
 CC given in T19001-726837 and which is able to hybridise to part of  
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)  
 CC sequences were obtained from 3'-directed cDNA libraries prepared  
 CC from various human tissues; synthesis of cDNA was initiated from the  
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-  
 CC untranslated sequence is unique to a particular mRNA species, almost  
 CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library  
 CC is constructed so as to reflect accurately the relative abundance of  
 CC different mRNAs in the particular tissue from which it was derived.  
 CC The appearance frequency of a given GS in a cDNA library can be  
 CC determined (esp. using primers and probes derived from the GS  
 CC sequences) as a means of diagnosing abnormal cell function or for  
 CC recognising different cell types.  
 SO Sequence 265 BP; 56 A; 50 C; 59 G; 91 T;

|    | Best Local Similarity | Matches                                                            | Conservative | Mismatches | Indels | Gaps |
|----|-----------------------|--------------------------------------------------------------------|--------------|------------|--------|------|
| QY | 1822                  | gtctggagcttgggtccggttgcacgctctgaatccacgaatctggagtcgaagcg           | 1881         |            |        |      |
| Db | 1370                  | gccccttcctcctgggacatgctctacgaccttaatccacgattttggagagccaaacaa       | 1311         |            |        |      |
| QY | 1882                  | gcgagatcacccagagttcagaagttccagacacgcctgcaccaaatctggtaaacctctct     | 1941         |            |        |      |
| Db | 1310                  | gtggatgacttgaggtgcagagcttcaaaacacccctggcccaaaatggtgaaccocatct      | 1251         |            |        |      |
| QY | 1942                  | ctctctaaactacaaaaaatctgaactgggttgggtggcggtgcctctgaatcccaagctactc   | 2001         |            |        |      |
| DJ | 1250                  | ctactctaaaaatgcaaaaaatctagctgggtgtggtgtgcacgaccttgaatccagctactc    | 1191         |            |        |      |
| QY | 2003                  | gggaagctcaggaagagttgaattgtttgaacctgggaagttgaggtcttcagtgagcagaga    | 2061         |            |        |      |
| Db | 1190                  | cggagagcttaggcacagagagatcattttgagcctgggagagtgagggttcagtgaggccgcaaa | 1131         |            |        |      |
| QY | 2062                  | tcacacccactgactctagccttgggttgcacagaagaagctctgtctctaaaaacaaacaa     | 2121         |            |        |      |
| Db | 1130                  | tggctccacactacactccagcctgggtgacacagcaagaagctctgtctcaaaaataataa     | 1071         |            |        |      |
| QY | 2122                  | aacaaacaaacaaacaaaa                                                | 2139         |            |        |      |
| Db | 1070                  | ataataataataaacccaga                                               | 1053         |            |        |      |

DP 1070 AATAAAATAAACCCAGA 1053

## RESULT 10

standard; DNA; 32367 BP.  
V35620.

Human SHOX (short stature)

lurher's syndrome; sho  
SHOX: bone dysplasia

Homo sapiens.

FD-09-APR-1998.  
PF-29-SEP-1997.

01.-OCT-1996; US-027633

Rao E, Rappold-hoerbrar  
NPT, 09-07-718-004

and treatment of human

Claim 19; Pages 51-67;

approximately 500 kb in

stature gene. These gen

variations show

and exons of the SHOX gene

and show as shown. W60573 human growth Defect

3 treatment of short stamens

Treatment of bone diseases with distal

02301 BP;

### Summary Match 6.



CC With MHC-linked immune response, suppressing a cell mediated or  
CC humoral immune response. It may specifically be used to treat  
CC delayed-type hypersensitivity, leishmaniasis, and immune disorders.  
SQ Sequence 1618 BP; 461 A; 369 C; 356 G; 432 T;

Query Match 5.9%; Score 236.4; DB 1; Length 1618;  
Best Local Similarity 80.7%; Pred. No. 8e-49;  
Matches 276; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1790 ccatgtttgtgctatataaacctttaaagcttgcggtggtccggtgctacgcc 1849  
DB 1137 CCAGCTGTATTATTAACCACTTAATTTGGTTACAGCGCGCGCGGCTACGCC 1196  
QY 1850 ttaataccagcaatttggagtcgagcgcgagatcactgaggtcagagttccag 1909  
DB 1197 TGTATCCAGCAGCTTTGGAGGCTGAGCGGCTGATCCTTGAGGTCAAGATTCTTA 1256  
QY 1910 accagcctgacccaataatgtgaacctctctactactaaatacaaaatlaactgggt 1969  
DB 1257 ACCAGCTGTGTAACATGTAAGTAACCCCGTCTACTATAAATAAATAATAGCGGGC 1316  
QY 1970 gtgtgtgctgctgtcgttaattcccaagctacgtcggaagtcgaggtgattttga 2029  
DB 1317 ATGCTGGCGCGCAGCTGTATCCAGCTACTTGGGAGGCTGAGGCAAGAAATTTGCTTGA 1376  
QY 2030 acctgggaagtgaggttgcagtcagcagagatcacacacactcactgagcttggtga 2089  
DB 1377 ACCCAGAGATGGAAGTTGCACTGAGCTGATATCATGAGCCCTTACTCCAGCTGGGTGA 1436  
QY 2090 cagagcaagactctgtctaaatacaaaatacaaaatacaaa 2131  
DB 1437 CAGAGCAAGACTCTGTCTCAAAAAATAAATAAATAAATAA 1478

RESULT 13

ID Q46958 standard; CDNA; 1618 BP.

AC Q46958;

DE 25-JAN-1994 (first entry)

KW Human cytokine synthesis inhibitory factor clone pH15C.

KW Mammalian cytokine synthesis inhibitory factor; CSIF; interleukin 10;

KW IL-10; immune system imbalance; human T cell; leishmaniasis;

KW rheumatoid arthritis; systemic lupus erythematosus; thyroiditis;

KW myasthenia gravis; insulin-dependent diabetes mellitus; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT cds 31..567

FT mat\_peptide /tag a

FT /tag b

FT /product= mature\_CSIF

PN US5231012-A.

PD 27-JUL-1993

PF 28-JUN-1988; 372667.

PR 28-JUN-1988; US-372667.

PR 20-DEC-1989; US-453951.

PR 06-AUG-1990; US-546235.

PR 20-JUL-1992; US-917806.

PA (SCHE) SCHERING CORP.

PI Bond MW; Moore KW; Mosmann TR; Vieira PJM;

DR WPI: 93-249726/31.

DR P-PSDB; R39714.

PT Genes and proteins encoding cytokine synthesis inhibitory factors

PT - useful in treating diseases associated with cytokine

PT imbalances, e.g. parasitic infections and auto-immune disorders

PS Claim 1; Fig 4; 23pp; English.

CC A human T cell cDNA library was screened with probes based on the

CC murine CSIF gene. Two clones carrying plasmids pH5C and pH15C were

CC identified. (These two expression vectors are claimed). The CSIF

CC polypeptide they encode inhibits synthesis of cytokines associated

CC with delayed type hypersensitivity responses. CSIF (also called IL-

CC 10) can be used to treat diseases associated with cytokine

CC imbalances, such as leishmaniasis and MHC-associated autoimmune  
CC diseases caused by excessive production of interferon-gamma, e.g.  
CC rheumatoid arthritis, SLE, IDDM, myasthenia gravis and thyroiditis.  
SQ Sequence 1618 BP; 463 A; 367 C; 356 G; 432 T;

Query Match 5.9%; Score 236.4; DB 1; Length 1618;  
Best Local Similarity 80.7%; Pred. No. 8e-49;  
Matches 276; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1790 ccatgtttgtgctatataaacctttaaagcttgcggtggtccggtgctacgcc 1849  
DB 1137 CCAGCTGTATTATTAACCACTTAATTTGGTTACAGCGCGCGGCTACGCC 1196  
QY 1850 ttaataccagcaatttggagtcgagcgcgagatcactgaggtcagagttccag 1909  
DB 1197 TGTATCCAGCAGCTTTGGAGGCTGAGCGGCTGATCCTTGAGGTCAAGATTCTTA 1256  
QY 1910 accagcctgacccaataatgtgaacctctctactactaaatacaaaatlaactgggt 1969  
DB 1257 ACCAGCTGTGTAACATGTAAGTAACCCCGTCTACTATAAATAAATAATAGCGGGC 1316  
QY 1970 gtgtgtgctgctgtcgttaattcccaagctacgtcggaagtcgaggtgattttga 2029  
DB 1317 ATGCTGGCGCGCAGCTGTATCCAGCTACTTGGGAGGCTGAGGCAAGAAATTTGCTTGA 1376  
QY 2030 acctgggaagtgaggttgcagtcagcagagatcacacacactcactgagcttggtga 2089  
DB 1377 ACCCAGAGATGGAAGTTGCACTGAGCTGATATCATGAGCCCTTACTCCAGCTGGGTGA 1436  
QY 2090 cagagcaagactctgtctaaatacaaaatacaaaatacaaa 2131  
DB 1437 CAGAGCAAGACTCTGTCTCAAAAAATAAATAAATAAATAA 1478

RESULT 14

ID V35620/C standard; DNA; 32367 BP.

AC V35620;

DE 07-SEP-1998 (first entry)

KW Human SHOX (short stature homeobox containing gene) gene sequence.

KW Homeobox domain; human growth gene; growth regulation; growth defect;

KW Turner's syndrome; short stature homeobox containing gene; SHOXa;

KW SHOX; bone disease; osteoporosis; calcium regulation; short stature;

KW transcription factor A; ss.

OS Homo sapiens.

PI K09814568-AL.

PI 09-APR-1998.

PI 29-SEP-1997; E05355.

PI 16-JAN-1997; EP-100583.

PI 01-OCT-1996; US-027633.

PI (RAPP/) RAPPOLD-HOERBRAND G.

PI Rao E; Rapppold-hoerbrand G.

DR WPI: 98-271719/24.

DR New human growth genes - used to develop products for the diagnosis

DR and treatment of human growth defects such as short stature, e.g.

DR Turner's syndrome

FS Claim 19; Pages: 51-67; 84pp; English.

CC This is the human SHOX gene sequence containing the PAR1 region. The gene

CC region corresponding to short stature has been identified as a region of

CC approximately 500 kb in the PAR1 region of the X and Y chromosomes. Three

CC genes in this region have been identified as candidates for the short

CC SHOX93 or HOX93). pT92 and SHOT (SHOX-like homeobox gene on chromosome

CC three). The SHOX gene has two separate splicing sites resulting in two

CC variations: SHOXa and SHOXb. The specification provides sequences of SHOX

CC (short stature homeobox-containing) genes SHOX E792, SHOXa, SHOXb, SHOT

CC and exons of the SHOX genes as shown in V35610 to V35621 and protein

CC sequences of the human growth protein transcription factor SHOXa, SHOXb

CC and SHOT as shown W60573 to W60575. The novel genes are responsible for

CC human growth. Defects in the genes can cause short stature, e.g.

CC Turner's syndrome. The products can be used to develop agents for the

CC treatment of short stature or other human growth disorders. The products



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|      |       |      |     |    |          |           |
|------|-------|------|-----|----|----------|-----------|
| C 23 | 449.2 | 11.2 | 454 | 51 | A1744242 | tr08a05.x |
| C 24 | 448   | 11.2 | 448 | 42 | A1088738 | ga16f11.x |
| C 25 | 448   | 11.2 | 448 | 48 | A1559614 | tg58c07.x |
| C 26 | 448   | 11.2 | 448 | 63 | A1983370 | w232g07.x |
| C 27 | 447.2 | 11.2 | 452 | 63 | AM008384 | wv54d05.x |
| C 28 | 447   | 11.1 | 447 | 44 | A1275445 | q168g06.x |
| C 29 | 447   | 11.1 | 448 | 44 | A1291764 | q168g06.x |
| C 30 | 444   | 11.1 | 448 | 45 | A1524277 | q128c03.x |
| C 31 | 444   | 11.1 | 444 | 47 | A1523044 | ar78c04.x |
| C 32 | 443.4 | 11.1 | 445 | 41 | A1017354 | ov09b09.x |
| C 33 | 443   | 11.1 | 443 | 49 | A1623147 | tu89c05.x |
| C 34 | 443   | 11.1 | 444 | 63 | AM006651 | wt06e04.x |
| C 35 | 442   | 11.0 | 444 | 28 | AM086290 | zn52h03.s |
| C 36 | 437.6 | 10.9 | 444 | 62 | A1887698 | wm17c11.x |
| C 37 | 435   | 10.9 | 435 | 43 | A1189262 | gc99h08.x |
| C 38 | 432   | 10.8 | 433 | 36 | AA630015 | ad45g01.s |
| C 39 | 431   | 10.8 | 431 | 34 | AA478704 | zv09f01.r |
| C 40 | 430.2 | 10.7 | 436 | 41 | A1056642 | oz18f08.x |
| C 41 | 429.4 | 10.7 | 434 | 40 | AA974061 | og05h09.s |
| C 42 | 424.4 | 10.6 | 440 | 31 | AA291974 | zt28e11.r |
| C 43 | 424.4 | 10.6 | 437 | 42 | A1087177 | oz59g12.x |
| C 44 | 424   | 10.6 | 424 | 61 | A1859926 | wm23e11.x |
| C 45 | 420   | 10.5 | 420 | 45 | A1367605 | q930c04.x |

## ALIGNMENTS

RESULT 1  
AI401218/c  
LOCUS  
DEFINITION  
AI401218 673 bp mRNA  
similar to NCI-CGAP\_Brn23 Homo sapiens cDNA clone IMAGE:2103714 3'  
LOCUS PRECURSOR ; mRNA sequence.  
CHAIN PRECURSOR ; mRNA sequence.

ACCESSION  
NID  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
AUTHORS  
TITLE

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BRGAP), Tumor Gene Index  
Unpublished (1998)  
On Apr 7, 1998 this sequence version replaced gi:3035192.

JOURNAL  
COMMENT

Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
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Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 816 Std Error: 0.00  
Seq primer: -400P from Gibco  
High quality sequence stop: 450.

FEATURES  
SOURCE  
Location/Qualifiers

1. 673  
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/db\_xref="taxon:9606"  
/clone="IMAGE:2103714"  
/clone\_lib="NCI CGAP\_Brn23"  
/tissue\_type="glioblastoma (pooled)"

/lab\_host="DH10B"  
/note="Organ: Brain; Vector: pRT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TCCTACCATCTGCAAGTGGAGAGCCGCCCATCTCTTTTCTTTTCTTTTCTTTT  
T33]; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pRT73 vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT

195 a 146 c 111 g 221 t

Query Match 15.6%; Score 627.4; DB 46; Length 673;  
Eest local similarity 96.1%; Pred No. 5.5e-107;  
Matches 643; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1156 ttccctccaatcttcctgacccctggcgaagattttaaagaatttggagaccgaatgat 1215  
DB 673 TTCGCGCCATTTCGTGATCCGTGCGCAGATTATTAAGAAATGGTTGAGACCAAAATGAT 614

QY 1216 gatactctgacctgggaagatgacacatctatggagaagcaaacgaaggaaccgac 1275  
DB 613 GATTCTTTCGACGAGGAAGATGACATCAATGAGAACCAACCAAGAGGAAATGGAC 554

QY 1276 tctgtagctgtagaagaacccctgagacccctcagtgatgagaaattattttt 1335  
DB 553 TCTGTAGTCTGTATGAAATCTGAAAGACAGCTCTCATGATGAGATATTATTTT 494

QY 1336 accctacgtgacccctgggaagattctccattccatttggatcgtggaaattat 1395  
DB 493 ACCCTACGCTGACCTTGGAGAAATCTTCCCATCTTCATTTGTTATCTGGAACTAT 434

QY 1396 taatggaaacggaacactctgcacatttaaaacagcagcctataagaccaggt 1455  
DB 433 TAAATGGAACGTAACCTACTGACCATTTAAACAGCAGCTCATTAAGCCACAGGT 374

QY 1456 cttaagttagtcgcgcacccgaaacaaataatggcgcttggagaagatgtg 1515  
DB 373 CTTTATGTTGAGTCGCGGACCAAAACATAAATATGCGGCTTTGAGAGAGGTG 314

QY 1516 gagtcatcttcattgaattataaagccagcagcttcaaataggaggacaagaaaa 1575  
DB 313 GAGTCACTTCTCATTTGATTAATAAGCCAGCGCTTCAATAGAGGACCAAGCAAAA 254

QY 1576 gtgatagtggtggagtaacttaacaagattgacacactccggagatctat 1635  
DB 253 GTGATGATGAGTGGAGTTAATCTTATCAGAGTTGTGACAACTTCTGAGGATCTAT 194

QY 1636 actgcttgcttctcttgcaacatgacaacatttatttggagggaaactattg 1695  
DB 193 ACTTGCTTGTCTCTTCTTGTGCAACATGAAACAAATTTATTGAGGAACTCATTTG 134

QY 1696 ggggtgcaatgctaatgcaacacttgagtcacaagaacatgtagaacaaatggata 1755  
DB 133 GGGTGCAAATGCTTAATGTCAAACTTGAGTCACAAAGAACATGTAGAAAAACAAATGATA 74

QY 1756 aaatctgatatgttggtagccattgaaccagttgttgcttataaactctt 1815  
DB 73 AAATCTGATATGATTTGTTGGATCTTATGACCAATGTTGTGGCTATTAAACTCTT 14

QY 1816 ttaacagtc 1824  
DB 13 TTGGCAGTC 5

RESULT 2  
A1768613/c  
LOCUS  
DEFINITION  
A1768613 624 bp mRNA  
EST  
28-JUN-1999  
WH24a04.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2381646 3'  
similar to SW:1131\_HUMAN P78552 INTERLEUKIN-13 RECEPTOR ALPHA-1  
CHAIN PRECURSOR ; mRNA sequence.



ACCESSION A1768613  
 NID 95235122  
 VERSION A1768613.1 GI:5235122  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 624)  
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 TITLE Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT On Dec 20, 1995 this sequence version replaced gi:1134640.

Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
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 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/dbp/image/image.html

Seq primer: -40UP from G1BCO  
 High quality sequence stop: 475.  
 FEATURES  
 source

1. 624  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /map="9"  
 /clone="IMAGE:2381646"  
 /clone\_lib="NCI-CGAP\_Kid11"  
 /lab\_host="DH10B"  
 /note="Organ: Kidney; Vector: p773D-Pac (Pharmacia) with  
 a modified polylinker. Site 1: Not I; Site 2: Eco RI;  
 Plasmid DNA from the normalized library NCI-CGAP\_Kid1 was  
 prepared, and ss circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive  
 hybridization reaction. The driver was PCR-amplified cDNAs  
 from a pool of 5,000 clones made from the same library  
 (clonids 132376-132391). 1456007-1456775, and  
 1500552-1502855). Subtraction by Bento Soares and M.  
 Fatima Bonaldo."  
 BASE COUNT 176 a 123 c 115 g 208 t 2 others  
 ORIGIN

Query Match 15.28; Score 609.4; DB 59; Length 624;  
 Best Local Similarity 99.48; Pred. No. 1.2e-103;  
 Matches 621; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 Oy 784 cagaatttttagcagatgcctattatgaagtagaagcacaacacagcag 843  
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 Db 624 CAGAAATTITAGCAATGCTTATATGAGTAGAAGCAATTAACGCCAATCTGAG 565  
 Oy 844 acacataatgtttctacgtcacaagagcctaattgagaattcagaattgagaagaat 903  
 |||||  
 Db 564 ACACATATATTTTCTACGCAAGAGCCTAAATGTAGATCCAGATTTGAGAGAAAT 505  
 Oy 904 gtgagagatcatctgtttcatgtgtccctgggtgtttctctgtatttgaacagtc 963  
 |||||  
 Db 504 GTGGAGATTCATCTTCTTCATGCTCCCTGGTGTCTTCTCTGATCTTGAACACAGTC 445  
 Oy 964 agataagagtcacaacaaatagttatgtcatagagtagacaacccctgagtaattgg 1023  
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 Db 444 AGATAAGAGTCACAACAAATTAATTAATGATGAGATGACAAACTCTGAGTAATGG 385  
 Oy 1024 agccaaagaatgagtagtaagtagcgaattccacactctacataacacattactc 1083  
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Dh 384 AGCCATGAAATGATATAGGTAAAGACGCAATTCACACTGTACATTAACCATGTTACTC 325  
 Oy 1084 attttcagtcagtcgctgcgagagtagcatcatagtaactcgtcttaacctaagaagctc 1143  
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 Db 324 ATTCTCCAGTACATGCTGCGAGGTGATCATTAATCTCTGCTTTACTT-AAAAGCTC 266  
 Oy 1144 agattatcatatccctccaatccctgcatacctcgtgccaagattttaagaagtgttga 1203  
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 Db 265 AAGATTATTATATTCCTCCCAATTCCTGATCCCTGCAAGATTTTAAGAATGTTTGA 206  
 Oy 1204 gaccagaatgtagtactctgctgactggaagaagtagacatctatgagaagcaaacga 1263  
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 Db 205 GACCGAATATGATGATCTGCACTGCAAGAGTACGACATCTATGAGAACCAACCAAG 146  
 Oy 1264 gaggaaacgactctgagtgctgatatagaagaacgtgagaagaagcctcagtagtga 1323  
 |||||  
 Db 145 GAGGATACCGACTGTGTAGTGTGATGAAACCTGAGAAAGCCTCTCAGTATGAGA 86  
 Oy 1324 taattatttttacttactgctgactgagaagattctccattccattgattat 1383  
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 Db 85 TAATTATTTTACTCTGCTGACTGAGATTCCTGCAATTCCTCATTTGTTAT 26  
 Oy 1364 ctgggaacttaataatgaaactg 1408  
 |||||  
 Db 25 CTGGGAATCTATTAATGAAACTG 1

REVISED 3  
 AA523414/c 596 bp mRNA EST 21-AUG-1997  
 LOCUS ng30a07.s1 NCI-CGAP\_C03 Homo sapiens CDNA clone IMAGE:936276 3'  
 DEFINITION mRNA sequence.  
 ACCESSION AA523414  
 NID 92264126  
 VERSION AA523414.1 GI:2264126  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 596)  
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 TITLE Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT On May 18, 1995 this sequence version replaced gi:810992.

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 Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,  
 M.F., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arraying: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/dbp/image/image.html

Insert Length: 841 Std Error: 0.00  
 Seq primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 472.  
 FEATURES  
 source

1. 596  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:936276"  
 /clone\_lib="NCI-CGAP\_C03"  
 /sex="pooled"  
 /tissue\_type="colon"  
 /lab\_host="DH10B"  
 /note="Vector: p773D-Pac (Pharmacia) with a modified  
 polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was prepared from 12 pooled bulk tumor samples and primed with a Not I - Oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTZ19 vector. Library went through one round of normalization.

BASE COUNT 207 a 135 c 103 g 151 t  
ORIGIN

Query Match 14.8%; Score 592.8; DB 34; Length 596;  
Best Local Similarity 99.7%; Pred. No. 1.5e-100;  
Matches 594; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3401 agaatattgttctctctgataagaatgagatattccttccagatatttataatt 3460  
DB 596 AGAATATTGTTCTCTCTGATGAGATGAGATTAATCTTCCAGATATTATATT 537  
QY 3461 ctgggaagcaaacacacatgcctccctcagcattttactgtatcctattagatgc 3520  
DB 536 CTGGGAAGCAAAACCCATGCCCTCCCTAGCCATTTTACTGTTATCTTATTGATGGC 477  
QY 3521 catgaagaagatgtgtgaattcccaacaacattatgtctgacatctatgcagcttg 3580  
DB 476 CATGAAGAAGATGCTGTGAATTCACAAACAATGATGCTGACATGACGTGG 417  
QY 3581 gaatgggaagtgatctcttcttccatccctctctcttcttcttcttcttcttcttct 3640  
DB 416 GAGTGGGGAAGTATCTTTTGTTCCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 357  
QY 3641 aaagggaggaagaaagaaatgagaaatgagaaatgagaaatgagaaatgagaaatg 3700  
DB 356 AAAGGGAGGAGGAAAGGAAAGTATGGAATACCTGTGGTGGTGGTGGTGGTGGTGG 297  
QY 3701 gagctcttgagagtggtctgtatcagtgattccctccctctgaggaatagtagct 3760  
DB 296 GAGCTCTTGAGGTGCTGTGATCATGATGATTCCTCATCCCTGGGAAATATGATGCT 237  
QY 3761 catttactgttttaagtgatcagcctatgtgagatttttcttcttcttcttcttcttct 3820  
DB 236 CATTACTGTTTATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 177  
QY 3821 gttcagagatggaattcttcttcttcttcttcttcttcttcttcttcttcttctt 3880  
DB 176 GTGTGAGAGAGTGAATCTTATCTTCTGCTGATGATGATGATGATGATGATGATGAT 117  
QY 3881 tgaaggagatgtgaacaatgttaacattttgtgtagcttcttcttcttcttcttctt 3940  
DB 116 TGAAGGATATGTGAACAATGTTACATTTTGTGTGATGATGATGATGATGATGATGAT 57  
QY 3941 gtttaacttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 3996  
DB 56 GTTAACTCTTATGAGAAAGCTGATTAATAATATGATGATGATGATGATGATGATGAT 1

RESULT 4  
AI888989/c  
LOCUS AI888989 627 bp mRNA EST 01-SEP-1999  
DEFINITION w116b01.x1 NCI CGAP Kid2 Homo sapiens cDNA clone IMAGE:2402953 3'  
similar to SW:1131\_HUMAN P78552 INTERLEUKIN-13 RECEPTOR ALPHA-1  
CHAIN PRECURSOR; mRNA sequence.

ACCESSION AI888989  
NID 95594153  
VERSION AI888989.1 GI:5594153  
KEYWORDS EST

SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished (1997)  
COMMENT On Jun 5, 1998 this sequence version replaced gi:3188446.

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Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Greg Lennon, Ph.D.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/btrp/image/image.html

Seq primer: -400p from Glibco  
High quality sequence stop: 388.

FSATRES  
source

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2402953"  
/clone\_lib="NCI-CGAP\_Kid2"  
/tissue\_type="2 pooled tumors (clear cell type)"  
/lab\_host="DH10B"  
/note="Organ: Kidney; Vector: pTZ19-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
Plasmid DNA from the normalized library NCI-CGAP Kid2 was  
prepared, and ss circles were made in vitro. Following HAP  
purification, this DNA was used as tracer in a subtractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(clones 1323912-1325831, 1471368-1472903 and  
1492104-1493255). Subtraction by Bento Soares and M.  
Retina Bonaldo."

BASE COUNT 172 a 137 c 108 g 210 t  
ORIGIN

Query Match 14.7%; Score 590.8; DB 62; Length 627;  
Best Local Similarity 98.6%; Pred. No. 3.4e-100;  
Matches 617; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 1135 aaaaagcctcaagattatctatccctcccaatccctcctcctcctcctcctcctcctcct 1194  
DB 627 AAAAGCTCAAGATTAATTAATCTCCATTCCTGATCCGATCTGGCAAGATTTTAAAGAA 568  
QY 1195 atgtttggagaccagatgatactctgtcactcgtgaagaagtaagacatcatgagaag 1254  
DB 567 ATGTTTGGAGACCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 508  
QY 1255 caaaccaaggaagaaacgactctgagtgctgataagaacactgaagaacccctctcg 1314  
DB 507 CAACCAAGAGGAAACCACTCTGTAGTGTGATGAAACCTGAAAGAAACCTCTCAG 448  
QY 1315 tgatgagataatttatttcttccctcactgtgaccttgaagaattcttccattctcc 1374  
DB 447 TGATGAGATTAATTAATTTTAATCTTCACTGAGCTTGAAGAATCTTCCATTCTCC 388  
QY 1375 attgttctcctgggaacttataatgaagaactgaagaactgaagaactgaagaactga 1434  
DB 387 ATTTGTTATCTGGAGACTTAATTAATGAAGAACTGAACCTGACCATTTTAAAAAAG 328  
QY 1435 cagctcataagagcccaagctcttattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1494  
DB 327 CAGCTATAAGACCCAGAGCTTTATGTTGATGCGGACGCAAAAATAAATAAATAG 268  
QY 1495 ggcgctttggagaggtgtgagtcactcattgaattataaagccagagcttca 1554  
DB 267 GCGGCTTTGGAGAGAGTGTGAGTATCTCATTAATTAATAAGCAAGCAAGCTTCA 208  
QY 1555 aactaaggagacaaagcaaaagtgatgagtagtggtgagtaattatcaagagtggtg 1614

| DB         | 207                                                            | AACTAGGGGACAAACACAACTGATGATGATGAGTGTATCTTATCTTATCAAGAGTGTG      | 148         |
|------------|----------------------------------------------------------------|-----------------------------------------------------------------|-------------|
| QY         | 1615                                                           | aaactctctgtggggaatctatactctgtgcttggctcttgggtgcaacatgaacaatttt   | 1674        |
| Db         | 147                                                            | ACAACTTCTGTGGGAGATCTATACTGCTCTTGTGTTCTTGTCACAACATGAACAAATTTT    | 88          |
| QY         | 1675                                                           | attttaggggaaccatctt-agggtgtcaatgct-aatgtcaacttgatgcacaaga       | 1732        |
| Db         | 87                                                             | ATTTTAGGGGACACTCATTGTTGGGGGTGCACAAATGCTAAATGTCAACTTGATGTCACAAAG | 28          |
| QY         | 1733                                                           | acatgtagaaaaacaaatgataaaa                                       | 1758        |
| Db         | 27                                                             | ACATGTAGGAACACCAATGAGTATAA                                      | 2           |
| RESULT     | 5                                                              |                                                                 |             |
| LOCUS      | AL036221                                                       |                                                                 |             |
| DEFINITION | AL036221                                                       | 673 bp                                                          | mrna        |
| KEYWORDS   | DKRZP5641I202.r1.564 (synonym: hfbr2)                          |                                                                 | EST         |
| ACCESSION  | AL036221                                                       |                                                                 | 27-SEP-1999 |
| NID        | 93405818                                                       |                                                                 | 27-SEP-1999 |
| VERSION    | AL036221.1                                                     | GI:5405818                                                      |             |
| KEYWORDS   | EST.                                                           |                                                                 |             |
| SOURCE     | human.                                                         |                                                                 |             |
| ORGANISM   | Homo sapiens                                                   |                                                                 |             |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  |                                                                 |             |
| AUTHORS    | Eutheria; Primates; Catarrhini; Hominiidae; Homo.              |                                                                 |             |
| COMMENT    | 1 (bases 1 to 673)                                             |                                                                 |             |
|            | Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and |                                                                 |             |
|            | Miemann, S.                                                    |                                                                 |             |
|            | EST (Duesterhoeft, et al.)                                     |                                                                 |             |
|            | Unpublished (1999)                                             |                                                                 |             |
|            | On Jun 22, 1998 this sequence version replaced gi:3246899.     |                                                                 |             |

**Contact:** Duesternhoeft A  
MIPS  
Am Klopferspitz 18a D-82157 Martinsried, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ): Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Qiagen within the cDNA sequencing consortium of the  
German Genome Project.  
No sl sequence available.  
This clone is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

| FEATURES   | SOURCE | Location/Qualifiers                               |
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|            |        | 1. .673                                           |
|            |        | /organism="Homo sapiens"                          |
|            |        | /db_xref="taxon:9606"                             |
|            |        | /clone="DKFZP5641202"                             |
|            |        | /clone_11b="564 (synonym: hfr2)"                  |
|            |        | /tissue_type="brain"                              |
|            |        | /dev stage="fetal"                                |
|            |        | /lab_host="X1-2blue"                              |
|            |        | /note="vector: pAMP1, Site_1: NotI, Site_2: SalI" |
| BASE COUNT |        | 199 a 148 c 154 g 168 t 4 others                  |
| ORIGIN     |        |                                                   |

| Query Match           | 14.3%          | Score 574.8                                                    | DB 61    | Length 673 |
|-----------------------|----------------|----------------------------------------------------------------|----------|------------|
| Best Local Similarity | 96.6%          | Pred. No. 3.2e-97                                              |          |            |
| Matches 650           | Conservative 0 | Mismatches 15                                                  | Indels 8 | Gaps       |
| Qy                    | 93             | ggggcgggcgggcgccgagcgtacggaactcagccactg-tgacaaattgagtg         | 151      |            |
|                       |                |                                                                |          |            |
| Db                    | 2              | ggggggggggggggcgccgcccgcctcaggaactcagccaccctgagacaaaatttgacgtg | 61       |            |
| Qy                    | 152            | tctctgttbaaacctcttcacagaaatattgacatgnaatcacccgggggaagccagtg    | 211      |            |
|                       |                |                                                                |          |            |
| Db                    | 62             | tctctgttbaaacacctcttcacagaaatattgacatgnaatcacccgggggaagccagtg  | 121      |            |

|    |     |                                                               |     |
|----|-----|---------------------------------------------------------------|-----|
| OY | 212 | caaatitgagctatggtatatttgatcttcttgccgcaacaagataaagaatggcc      | 271 |
| DB | 122 | CAATTGTAGCTATAGTATTTTTNGTCAATTTTGCCGCAACAAGATAGAAATAATGCTC    | 181 |
| OY | 272 | cggaaactcgtctgtccatataagaataccctgaatgagaagattgctcgaatgggt     | 331 |
| DB | 182 | CGGAATACCTGTGTTCAATAGTAAGTACCCCTGATGAGAGATTGTGCTCAAGTGGGGT    | 241 |
| OY | 332 | cccagttgagcacaatagagagtgagaaccttagcatlttggttgaataatgcatctac   | 391 |
| DB | 242 | CCCGATGTAGACCAACAAGAGAGTGAAGAGCTAGCATTTTGTGTGAATAATCATCTCAC   | 301 |
| OY | 392 | ccccgagatgagtcctcgtgagctgtcgttgactgaactcaatgcatlttgccacaactga | 451 |
| DB | 302 | CCCCAGAAGGATACCTGAGTCTGCTGTAGCTGAGCTTCAATGATTTTGGCACAACCTGA   | 361 |
| OY | 452 | gtcacatgaattgtcttcttgctcctc-ggaaggaaataccagtcgccgacaactaact   | 510 |
| DB | 362 | GCTCATGTAAGTGTCTTGCTGGCTCCCTGGGAAGAAATACAGTCCCGACATACTACTAG   | 421 |
| OY | 511 | ctctactattggccagagaagcctggaanaaatcatcaatgtgaaaaacatctttagaga  | 570 |
| DB | 422 | CTTACTATTGGCAGAGAGCTTGAAAAA-TCATCAATAGTAAAAACATCTTTAANAGA     | 480 |
| OY | 571 | ggcaataacttggtttcttcttgatctgacacaagaatgagaatccagtttttgaaga    | 630 |
| DB | 481 | GGCCCAATCTTTGGTGTGTTCTTGTGATCTACCAAAATGAAGATTCACATTTTGAACAA   | 540 |
| OY | 631 | cacagt-g-tccaataatggtcaagagataatgcaagaaaaatlaaacctccaatc-     | 688 |
| DB | 541 | CACATGTGTCACAATATAGTCAAGATATATGAGGAAAAAATTAAACATCTTCAANT      | 600 |
| OY | 688 | -atagtgcctttaaactcccggtgtgaaacctgatacctccacatatca-aaaccttcct  | 745 |
| DB | 601 | ATAGTGTCTTAACTTCCGCTGGAAGCTGATCTCCACATATATTANNAAACCTCTCT      | 660 |
| OY | 746 | tucacaatgatga 758                                             |     |
| DB | 667 | TCACAGTATGA 673                                               |     |

| RESULT     | C                                                                                                              | EST           | 24-AUG-1999                                                       |
|------------|----------------------------------------------------------------------------------------------------------------|---------------|-------------------------------------------------------------------|
| AI816791/c | AI816791                                                                                                       | 571 bp        | RNA                                                               |
| LOCUS      | W34409.x1                                                                                                      | NCI CGAP R1d2 | Homo sapiens                                                      |
| DEFINITION | similar to SM:U3131.HUMAN                                                                                      | P78552        | INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR ;, mRNA sequence. |
| ACCESSION  | AI816791                                                                                                       |               |                                                                   |
| ALT        | 95435870                                                                                                       |               |                                                                   |
| VERSION    | AI816791.1                                                                                                     | GI:5435870    |                                                                   |
| KEYWORDS   | EST.                                                                                                           |               |                                                                   |
| SOURCE     | human.                                                                                                         |               |                                                                   |
| ORGANISM   | Homo sapiens                                                                                                   |               |                                                                   |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Euthelia; Primates; Carnivora; Hominoidea; Homo. |               |                                                                   |
| AUTHORS    | 1 (bases 1 to 571)                                                                                             |               |                                                                   |
| TITLE      | NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .               |               |                                                                   |
| JOURNAL    | National Cancer Institute, Cancer genome Anatomy Project (CCAP), Tumor Gene Index                              |               |                                                                   |
| COMMENT    | Unpublished (1997)                                                                                             |               |                                                                   |
|            | On Jun 5, 1998 this sequence version replaced gi:3186971.                                                      |               |                                                                   |

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Tissue Procurement: Christopher Moskauk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Centre  
Clone distribution: NCI-CGAP clone distribution information can  
be found through the I.M.A.C.E. Consortium/BLNL at:  
[www-bio.liml.gov/dbfp/image/image.html](http://www-bio.liml.gov/dbfp/image/image.html)



|||||  
 Db 246 ACATCTTAGAGAACGCCATACCTTGTGTTGCTTGTGATCTGACCAAGTGAAGAT 305  
 QY 617 ccagtttgaacacacagatgctcaataatggtcaagataatgcggaaaaatcaac 676  
 Db 306 CCAAGTTTGAACAACAGAGTGTCCAAATATGCTCAAGATGAAGCAAGAAAAATTAAC 365  
 QY 677 caccctcatatagtgcccttaactcccggtgaaacctgacccccaataaa 736  
 Db 366 CACTCTTCATATATAGTCTTAACTTCCGTGGAACCTGATCCTCCACATTTTAAA 425  
 QY 737 acctctctccacaatgacatataatgcaatggaagacccaagaatttata 796  
 Db 426 ACCTCTCTTCCAAATGATGACCTATATGCAATGGAGAAATCCACAGATTTATTA 485  
 QY 797 gcaagatgctattatgtagaagtagaagtaacaaagccaaactgaga 844  
 Db 486 GCAGATGCTCTATTTTATGAGTAGAGTCAATACACCAACTGAGA 533

RESULT 8  
 A1887705/c 521 bp mRNA EST 01-SEP-1999  
 LOCUS wml7d11.x1 NCI\_CGAP\_Ut4 Homo sapiens cDNA clone IMAGE:2436213 3'  
 DEFINITION mRNA sequence.  
 ACCESSION A1887705  
 NID G5592869  
 VERSION A1887705.1 GI:5592869  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 521)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 On Jun 5, 1998 this sequence version replaced gi:3187155.

JOURNAL  
 COMMENT

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 Tel: (301) 496-1350  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 www-bio.lnl.gov/bdip/image/image.html

Seq primer: -40UP from Gibco  
 High quality sequence stop: 408.  
 Location/Qualifiers  
 1. 521  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /map="21q:56cm"  
 /clone="IMAGE:2436213"  
 /clone\_lib="NCI\_CGAP\_Ut4"  
 /tissue\_type="serous papillary carcinoma, high grade, 2  
 pooled tumors"  
 /lab\_host="DH10B"  
 /note="Organ: uterus; Vector: PCMV-SPORT6; Site: 1; Salt;  
 Site: 2; Note: Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.48 kb. Life Technologies catalog #:  
 11542-016"

BASE COUNT 179 a 121 c 92 g 129 t  
 ORIGIN  
 Query Match 13.0%; Score 521; DB 62; Length 521;

Best Local Similarity 100.0%; Pred. No. 3, 1e-87;  
 Matches 521; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3476 cagcctcccccttagcatttttaccgttaccattatagatccatgaaagagatgc 3535  
 Db 521 CATGCCCTCCCTAGCCATTTTACCTGTTATCCATTATTAATGCGCATGAAGAGATGCT 462  
 QY 3536 gtgaattcccaacaacatttgatgacagtcacatgacatgagtgagtgaggaagat 3595  
 Db 461 GTGAATATCCCAACAACATTTGATGCTGACAGTCATCATCTGCGAGTGGAGATGAT 402  
 QY 3595 cttgttcccatctctctcttttaagcagtaaatagctgaggaagaaagaggaag 3655  
 Db 401 CTTTGTTCACATCTCTCTCTTTAGCAGTAAATACCTGAGGAAAGAGGAGAAAG 342  
 QY 3656 gaagttatggaaataactggtggtgtgtatccctagtgcttggagccttggaggtg 3715  
 Db 341 GAAGTTATGGAAATACCTGTGTGTGTGTATCCCTAGGCTTGGAGGCTCTTGAGAGTG 282  
 QY 3716 tctgtacagtggaattcccatcccccctgtgggaattagtagctcattactgtttag 3775  
 Db 281 TCTGTATCAGTGGATTTTCCATCCCTGTGTGGAAATAGTAGCTCATTTACTTTTAG 222  
 QY 3776 gtctagcctatgtgatttttcttcaacacacacacacacacacacacacacacac 3835  
 Db 221 GTCTAGCCTATGAGATTTTCTCTTACATACCTTAACCAACCAACCAAGTGTGAGATG 162  
 QY 3836 ttcttattcttctgttcaatgaatttttcccttcaatcctgagcctgaggaagatgtga 3895  
 Db 161 TTTCTATCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 102  
 QY 3896 aacaatttcaactttttgttgaatcttcaacacacacacacacacacacacacacacac 3955  
 Db 101 AACCATTTTAACTTTTGTGATGCTTCAACCAAGGATTTTCTGTACTTTCTATA 42  
 QY 3956 ggaagcttgagtaaatataatgtcttcttctgtatgtca 3996  
 Db 41 GGAAGCTTGATTAATTAATATATGTCTTTTGTATGTCA 1

RESULT 9  
 A4669035/c 507 bp mRNA EST 20-NOV-1997  
 LOCUS ab88g12.s1 Stragene lung (#937210) Homo sapiens cDNA clone  
 DEFINITION IMAGE:854086 3', mRNA sequence.  
 ACCESSION A4669035  
 NID 52630534  
 VERSION A4669035.1 GI:2630534  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 507)  
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Getzel, G., Jost, S.,  
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,  
 Martin, J., Moore, B., Schellenberg, K., Stepien, M., Tan, F.,  
 Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
 WashU-NCI human EST Project  
 Unpublished (1997)  
 On Nov 6, 1997 this sequence version replaced gi:937221.

TITLE  
 JOURNAL  
 COMMENT

Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: estewatson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Seq primer: -40m13 fwd. RT from Amersham  
 High quality sequence stop: 455.  
 Location/Qualifiers

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source
1. 507
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:854086"
/clone_1lb="Stratagene lung (#937210)"
/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: lung; Vector: pluscript SK-; Site: 1;
EcORI; Site 2: XhoI; Cloned unidirectionally. Primer:
0.190 dt. normal lung. Average insert size: 1.0 kb;
uniZAP XR vector; -5' adaptor sequence: 5' GAATTCGACGAC
3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"

BASE COUNT 176 a 120 c 84 g 127 t
ORIGIN

Query Match 12.6%; Score 507; DB 37; Length 507;
Best Local Similarity 100.0%; Pred. No. 1.2e-84;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3490 gccattttactgtatccatttagatggccatgaagagatgcttgaattcccaac 3549
|||||
Db 507 gccattttactgtatccatttagatggccatgaagagatgcttgaattcccaac 448
|||||
QY 3550 aaacattgagtcagcagtcagtcagtcaggagtgaggagtgatctttgtccatc 3609
|||||
Db 447 AAACATTGATCTGACAGTCATGAGCTCGAGAGTGGGAGAGTATCTTTGCCATC 388
|||||
QY 3610 ctctctttttgacgtaaaatagcttgaggaggaagagagagagagagagagagat 3669
|||||
Db 387 CTCTCTTTTAGCAGTAATAAGCTGAGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGT 328
|||||
QY 3670 acctgt 3729
|||||
Db 327 ACCTGT 268
|||||
QY 3730 ttcccatccctgttggaatagtagtgatcattctgttttaggttagctatgtg 3789
|||||
Db 267 TTTCCCATCCCTGTGGGAAATGTAGTGGCTCATTTACTGTTTAGGCTGTGCTATGTG 208
|||||
QY 3790 gatttttcccaatccttagaaccacagttcagagatgagatcttctatcttctg 3849
|||||
Db 207 GATTTTTCCTACATACCTTAGCAACCCAGGTCTAGAGATGTAATCTTATCTTTCG 148
|||||
QY 3850 ttccagtttaagtttccctcctcctcctcctcctcctcctcctcctcctcctcct 3909
|||||
Db 147 TTCACTTAAGTTTTCCTCCTCATCTGGGCACTGAAGGATGTGGAACAATGTTACAT 88
|||||
QY 3910 ttctgttagcttcaaccagagatgttctgttttaactcttataagaaagcttgagta 3969
|||||
Db 87 TTTTGGAGAGCTTTCACACGAGGATGTTTCTGTTAACTTCTTATAGGAAGCTTGAGTA 28
|||||
QY 3970 aataaataattgtcttttttgaatgta 3996
|||||
Db 27 AAATAAATAATGTCTTTTGTATGTCA 1
|||||

RESULT 10
AI436787 504 bp mRNA EST 30-MAR-1999
LOCUS AI436787c
DEFINITION th82108.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125191
3', mRNA sequence.
ACCESSION AI436787
NID 9428448
VERSION AI436787.1 GI:4284488
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 504)
AUTHORS NC1-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

```

```

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
On May 18, 1998, this sequence version replaced gi:318159.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 1009 std Error: 0.00
Seq primer: -40UP from gibco
High quality sequence stop: 465.
Location/Qualifiers
1. 504
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="917A12; 1; 858608; 902A12; 960E05; 1q31.3-1q32.1;
1q31.3-1q32.1; 1q31.3-1q32.1; 1q31.3-1q32.1"
/clone="IMAGE:2125191"
/clone_1lb="Soares_NHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(pharmacia) with a modified polylinker; Site: 1: Not I;
Site: 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBH, pregnant uterus
NBHPU, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

BASE COUNT 176 a 119 c 83 g 126 t
ORIGIN

Query Match 12.6%; Score 504; DB 46; Length 504;
Best Local Similarity 100.0%; Pred. No. 4.5e-84;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3492 cactttactgtatccatttagatggccatgaagagatgcttgaattcccaaca 3551
|||||
Db 504 CATTTTTACGTTATCTTTTAGATGCCATGAAGAGATCTGGAATTCACAA 445
|||||
QY 3552 acctatgtctgacagtcagtcagtcaggagtgaggagtgatctttgtcccatc 3611
|||||
Db 444 ACATTAATGCTGACATGATGAGTGTGGAGTGGGAGAGTATCTTTGTCCATCT 385
|||||
QY 3612 ctctctttagcaataaagctgaagaggaagaggaaggaaggaatgaggaatc 3671
|||||
Db 384 CTCTTTTACGATTAATAATAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 325
|||||
QY 3672 ctgt 3731
|||||
Db 324 CTGT 265
|||||
QY 3732 tcccatccctgttggaatagtagtgatcattctgttttaggttagcctatgtgga 3791
|||||
Db 264 TCCCATCCCTGTGGGAAATGTAGTGCATTTACTGTTTAGGCTTAGCCTATGTGA 205
|||||
QY 3792 ttttccctaacatcctaagcaaacacagtgctgaagatggaattcttattcttctgt 3851
|||||
Db 204 TTTTTCCTTAACCTAAGCAAAACCGATCTCAGAGATGTAATCTTATTTCTTTCGT 145
|||||
QY 3852 cagtttaagtttccctcctcctcctcctcctcctcctcctcctcctcctcctcct 3911
|||||
Db 144 CACTTAAGTTTTCCTTCATCTGGGCACTGAAGGATGTGGAACAATGTTACATTT 85
|||||
QY 3912 ttgttagcttcaaccagagatgttctgtttaactcttataagaaagcttgagtaa 3971
|||||

```

Db 84 TTGGTACTCTCAACGAGGATGTTCTGTTAACTTTAAGAAAGCTTGAGTAA 25  
 Oy 3972 ataatatgtcttttgcctatgc 3995  
 Db 24 ATAAATTTCTCTTTTGTATGTC 1

RESULT 11  
 A1792304 501 bp nrna EST 02-JUL-1999  
 LOCUS A1792304  
 DEFINITION ah14e02.y5 Gessler Wilms tumor Homo sapiens cDNA clone  
 IMAGE:1156534 5' similar to contains Alu repetitive element; mRNA  
 sequence.  
 ACCESSION A1792304  
 NID 95340020  
 VERSION A1792304.1 GI:5340020  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 501)  
 NCI/NIH-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute / National Institute of Dental Research,  
 Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 Unpublished (1997)  
 On Jun 5, 1998 this sequence version replaced gi:3187393.  
 Other ESTs: ah14e02.x5  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 This clone is available royalty-free through LNLN; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 This read is a RESEQUENCE of a previously sequenced human clone  
 Original clone citation: see original entry for original citation  
 Information  
 This 5' resequenced clone has no previous 5' data to verify this  
 new read against  
 Seq primer: -40RP from G1bco  
 High quality sequence stop: 434.  
 Location/Qualifiers  
 1..501  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /map="1"  
 /clone="IMAGE:1156534"  
 /clone\_lib="Gessler Wilms tumor"  
 /sex="pooled (6)"  
 /lab\_host="DH10B"  
 /note="Vector: pSPORT1; Site\_1: SalI; Site\_2: NotI; RNA  
 was prepared from a pool of 6 anonymous Wilms' tumor RNAs.  
 RNA was prepared by acid-phenol, followed by one round of  
 oligo dT selection. cDNA library preparation was with  
 the BRL/Life Tech. Superscript plasmid system. An  
 oligo-dT NotI primer for first strand synthesis generated  
 ggcggcgccct(n) at the 3' end of the clones. A 5' SalI  
 adaptor was used with sequence 5'-gtgaccgacgcgcg-3'.  
 Resulting cDNAs were size selected (average size 2 kb),  
 NotI digested, and ligated into NotI/SalI-cut pSPORT1.  
 Library was constructed by Dr. Manfred Gessler."

BASE COUNT 146 a 118 c 124 g 111 t 2 others

ORIGIN

Query Match 12.4%; Score 499; DB 60; Length 501;  
 Best Local Similarity 99.6%; Pred. No. 3,8e-83;  
 Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1815 tttaacagctggcgctggcgctggcgctgaacgcttaacgaggaattggagcttc 1874  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 TTTTACAGTGTGGGCTGGGCTGGGCTGGGCTGGGCTTTAATCCAGCAATTTGGGACTCC 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Oy 1875 gaggcgaggatcagatcagagctcagagctcagaccagcctgaccacaaatggtgaac 1934

Db 61 GAGGCGGCGGAGTACCTCGAGGTCCAGAGTCCAGACCACTGACCAAAATGTTAAAC 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Oy 1935 ctctctctactaaactaaactaaactaaactaaactaaactaaactaaactaaactaa 1994  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 CTCCTCTCTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAA 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Oy 1995 gctactcggaagctgagcgagctgagctgagctgagctgagctgagctgagctgag 2054  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 181 GCTACTCGAGACCTAGAGAGTGAATTTTGAACCTGGAGAGTGGAGAGTGGAGTGA 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Oy 2055 gctgagatcacacacacacacacacacacacacacacacacacacacacacac 2114  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 GCAGAGATCACACACACACACACACACACACACACACACACACACACACACACAC 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Oy 2115 aaaaacacacacacacacacacacacacacacacacacacacacacacacacac 2174  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 AAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAAC 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Oy 2175 aacagatctctctctctctctctctctctctctctctctctctctctctctctct 2234  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 361 ACAGCATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Oy 2235 agaaaacacacacacacacacacacacacacacacacacacacacacacacacac 2294  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 421 AGAAAAACACAGAGGACAGCTCTTGCACAGACCTTCAAGCATTNTAGCTGTAGN 480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Oy 2295 gcaatgaggtgaatgacac 2315  
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 Db 481 GCAGTGGAGGTAGATGATGATC 501  
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RESULT 12  
 AA398286/c 498 bp mRNA EST 12-AUG-1997  
 DEFINITION z160d08.sl Soares-testis\_NHT Homo sapiens cDNA clone IMAGE:726735  
 3' mRNA sequence.  
 ACCESSION AA398286  
 NID 92051395  
 VERSION AA398286.1 GI:2051395  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 498)  
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,  
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,  
 Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,  
 White, Y., Wylie, T., Waterston, R. and Wilson, R.  
 WashU-Merck EST Project 1997  
 Unpublished (1997)  
 On Sep 12, 1996 this sequence version replaced gi:1289000.

TITLE  
 JOURNAL  
 COMMENT

CONTACT: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu  
 This clone is available royalty-free through LNLN; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 788 Std Error: 0.00  
 Seq primer: 41m13 fwd. ET from Amersham  
 High quality sequence stop: 406.  
 Location/Qualifiers  
 1..498  
 /organism="Homo sapiens"  
 /db\_xref="GDB:5923646"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:726735"  
 /clone\_lib="Soares-testis\_NHT"  
 /sex="male"

FEATURES  
 source

/lab\_host="DH10B"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
 was prepared from mRNA obtained from Clontech  
 Laboratories, Inc., and primed with a Not I - oligo(dT)  
 primer [5']  
 TGTACCAATCTGAAGTGGAGCGCGCCCAATTTTCTTTT 3']  
 Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT73 vector. Library  
 went through one round of normalization to Cot5, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 166 a 118 c 83 g 131 t

ORIGIN

Query Match 12.0%; Score 482.8; DB 33; Length 498;  
 Best Local Similarity 99.4%; Pred. No. 3.9e-80;  
 Matches 495; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

3510 attagatgcatgaagagatgctgtgaattcccaacaacattgctgacagtc 3569  
 |||||||  
 Db 498 ATTAGATGCCATGAAGAGATGCTGTGAATTTCCACAAACATTGATGCTGACAGTC 439  
 |||||||  
 QY 3570 atgcaatctggagagtgagagatgctgtccatccctctctcttaagcagtaaaa 3629  
 |||||||  
 Db 438 ATGCACTCTGGAGTGGGAGATGATCTTTGTTCCATCTCTCTTTTACAGATMAA 379  
 |||||||  
 QY 3630 taactaaggagagagagagagagagagagagagagagagagagagagagagag 3689  
 |||||||  
 Db 378 TACCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 319  
 |||||||  
 QY 3690 ctgagcttgaggagctcttgaggagctgtctatcagctgagttccca-tcccctgtggga 3748  
 |||||||  
 Db 318 CTAGGCTTGGAGCTCTTGAGAGTGTCTATCAGTGAATTTCCACCTCCCTGGGGA 259  
 |||||||  
 QY 3749 aattagtaggcttacttactgttttaggtctagcctatgtgagatttttccataacacc 3808  
 |||||||  
 Db 258 AATTAGTAGGCTCATTTACTGTTTGTAGGTCTACCTATGTGGATTTTTCCTAACATACC 199  
 |||||||  
 QY 3809 taagcaaacccagctgtcagagatgtaattcttcttctgctcagcttaagttttccct 3868  
 |||||||  
 Db 198 TAAGCAACCCAGTGTGAGATGATGTAATTTTATTTCTTGTTCAGTAAATTTTCCCT 139  
 |||||||  
 QY 3869 tcatctggagcactgaaagagatgtgaacaagttaacatttttgtagcttaacca 3928  
 |||||||  
 Db 138 TCATCTGGGAGCTGAAGGATATGTGAACATGTAACTTTTGGTAGTCTTCAACCA 79  
 |||||||  
 QY 3929 gggatgtgttctgttaacttcttaagagagcttgagtaaaataaatatgtctttt 3988  
 |||||||  
 Db 78 GGGATGTGTCTGTTAACCTCTTAAGAGAAAGCTTGAATAAATAATATGCTTTT 19  
 |||||||  
 QY 3989 gtagtcaccccaaaaaa 4006  
 |||||||  
 Db 18 GTATGTACCCCAAAAAA 1

RESULT 13  
 A1141080 478 bp mRNA EST 29-OCT-1998  
 LOCUS A1141080/c g23cell.x1 Soares\_fetal\_lung\_NBH19W Homo sapiens cDNA clone  
 DEFINITION IMAGE:1739756 3', mRNA sequence.  
 ACCESSION A1141080  
 NID 93648537  
 VERSION A1141080.1 GI:3648537  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE  
 AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

JOURNAL Tumor Gene Index  
 Unpublished (1997)  
 COMMENT On Jan 19, 1998 this sequence version replaced gi:2285777.

Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 1857 Std Error: 0.00  
 Seq Primer: 40m13 fwd. Et from Amersham  
 High quality sequence stop: 444.

FEATURES  
 Location/Qualifiers  
 1..478  
 source

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1739756"  
 /clone\_lib="Soares\_fetal\_lung\_NBH19W"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: lung; Vector: pT73D (Pharmacia) with a  
 modified polylinker. Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was ligated with a Not I - oligo(dT) primer  
 [5']-TGTACCAATCTGAAGTGGAGCGCGCCCAATTTTCTTTT 3']  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M. Fatima Bonaldo. This library was constructed  
 from the same fetus as the fetal heart library, Soares  
 fetal heart NBH19W."

BASE COUNT 162 a 115 c 79 g 122 t

ORIGIN

Query Match 11.9%; Score 477; DB 42; Length 478;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-79;  
 Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3520 ccattgaaggagtgctgtgaattcccaacaacattgctgacatgcagcttg 3579  
 |||||||  
 Db 478 CCATGAAGGAGTGTGTGAATTTCCCAACAACATGTATGCTGACATGACAGTGTG 419  
 |||||||  
 QY 3580 ggaatggagagagtgatctttgtccatccctctctttagcagtaaaatagctgagg 3639  
 |||||||  
 Db 418 GGAGTGGGAGATGATCTTTTGTCCATCCTCTTTTACAGTAAATATGCTGAGGG 359  
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 QY 3640 aaaaaggagagagagagagagagagagagagagagagagagagagagagagag 3699  
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 Db 358 AAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 299  
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 QY 3700 ggaactcttgaggagtgctgtatcagtgattcccatccctctgtggagaaatagtagc 3759  
 |||||||  
 Db 298 GGAGCTTGGAGAGTGTCTGTATCAGTGTGATTTCCATCCCTGTGGGAAATTAATAGGC 239  
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 QY 3760 tcattacgttttagtgcataccatgtgatttttccctaacaataagcaaacacc 3819  
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 Db 238 TCATTACGTTTTAGTGTCTAGCTATGTGATTTTTCCTACACTTAAGCAAAACC 179  
 |||||||  
 QY 3820 agtgcagagatgttaattcttcttctgtcagtaagttttccctcatctgggca 3879  
 |||||||  
 Db 178 AGTGCAGAGATGTAATCTTAATCTTTCGTAAGTAAATTTTCCCTCATCTGGGCA 119  
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 QY 3880 ctgaaggagatagtgaaacaatgttaacattttgtgtgcttcaacagagatgttctc 3939  
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 Db 118 CTGAAGGAGTATGTAAACATGTAACTTTTGTGTGCTCTTCAACAGGAGATGTTTC 59  
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 QY 3940 tgttaactctttagagagagagagagagagagagagagagagagagagagagagagag 3996  
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 Db 58 TGTTAACCTCTTAAGAGAAAGCTTGAATAAATAATATGCTTTTGTATATCA 2



RESULT 14  
AA071468/c 507 bp mRNA EST 01-FEB-1997  
LOCUS 2e8f04.s1 Soares fetal heart NBH19W Homo sapiens cDNA clone  
DEFINITION IMAGE:366079 3', mRNA sequence.  
ACCESSION AA071468  
NID 91578899  
VERSION AA071468.1 GI:1578899  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 507)  
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chapelli, B.,  
Chissoe, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W.,  
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,  
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rikkin, L.,  
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,  
Trevaaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.,  
and Marra, M.  
TITLE Generation and analysis of 280,000 human expressed sequence tags  
JOURNAL Genome Res. 6 (9), 807-828 (1996)  
MEDLINE 97044478  
COMMENT On Sep 12, 1996 this sequence version replaced gi:1292034.

CONTACT: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.jnl.gov) for further information.  
Insert Length: 617 Std Error: 0.00  
Seq primer: 40M13 fwd. from Amersham  
High quality sequence stop: 424.  
Location/Qualifiers

# FEATURES

1..507  
/organism="Homo sapiens"  
/db\_xref="GDB:1282783"  
/db\_xref="taxon:9606"  
/clone="IMAGE:366079"  
/clone\_lib="Soares\_fetal\_heart\_NBH19W"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: heart; Vector: pT73D (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTCACATGTGAGTGGAGCGCCGACATCTTTTCTTTTCTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library was constructed by  
M.Fatima Bonaldo. This library was constructed from the  
same fetus as the fetal lung library, Soares fetal lung  
NBH19W."

BASE COUNT 174 a 117 c 84 g 129 t 3 others  
ORIGIN

Query Match 11.9%; Score 476.8; DB 28; Length 507;  
Best Local Similarity 98.6%; Pred. No. 5e-79; 5; Indels 2; Gaps 2;  
Matches 500; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 3492 cattttactgtatcatttta-gatggcattgaagagatgctgtgaattcccaaca 3550  
|||||  
DB 507 CATTTTACTGTATCCCTATTAAAGATGACATGAAGAGATGCTGAATCCCAACA 448  
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QY 3551 aacattgacgcagacatcatcagctcgtggagtggtgggaagatgattcttctccatcc 3610  
|||||

DB 447 AACATTGATGCTGACAGTCATGCGAGTGGGAGATGATCTTTTGTCCATCC 388  
QY 3611 tctctcttagcagtaaaatagcttgaggaaaaggaaaaggaattatgggaata 3670  
|||||  
DB 387 TCTCTCTTAGCAGTAAATAGTGTGAGGGAAGAAANGAAGAAAGATTAAGGAAATA 328  
|||||  
QY 3671 ccttggtggttgatgaccccttaggtcttggaagctcttggaaggtgtctglatcagtggat 3730  
|||||  
DB 327 CCTGTGTGTGTGTGATCCCTAGTCTTGTGAGACTCTTGAGAGGTGCTGATAGTGAAT 268  
|||||  
QY 3731 ttccc-accctcgttggaatattagagctcattacggttttagtctagcctatgtg 3789  
|||||  
DB 267 TTCGCATCCCTGCTGGGAATAGAGCTCATTTTACGTTTACGCTAGGCTATGTC 208  
|||||  
QY 3790 gatttccctacacatcattacgaaccacagctgacagatggttaattcttctcttg 3849  
|||||  
DB 307 GATTTTCTTCAACATACCTAACCAACCCAGTGTAGATGATTTCTTATCTTTG 148  
|||||  
QY 3850 ttccgttaagtttccctcattcctgacactggaagagatgtaaacatgttaacat 3909  
|||||  
DB 147 TTCAGTTAGTTTTCCTTCATCTGCGCATGAGGATATGTGAACATGTTAACAT 88  
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QY 3910 ttctgtatcttcaaccagggatgttctgttactcttataggaaagctttagta 3969  
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DB 87 TTTTGTAGCTTTCACACGAGGATTTTCTGTTTACTTCTTATAGGAAGCTTGAGTA 28  
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QY 3970 aacaaatattgtcttcttctgtatgtca 3996  
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DB 27 AATATATATGTCTTTTGTATGTCA 1  
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RESULT 15  
AA11324/c 485 bp mRNA EST 17-MAY-1997  
LOCUS 2v79b11.s1 Soares ovary tumor NBHOT Homo sapiens cDNA clone  
DEFINITION IMAGE:75037 3', mRNA sequence.  
ACCESSION AA11324  
NID 32068864  
VERSION AA11324.1 GI:2068864  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 485)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Getsel, G., Jost, S.,  
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,  
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theisling, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
WashU-Merck EST Project 1997  
Unpublished (1997)  
On Sep 12, 1996 this sequence version replaced gi:1406977.

CONTACT: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.jnl.gov) for further information.  
Seq primer: 41m13 fwd. ET from Amersham  
High quality sequence stop: 467.  
Location/Qualifiers

1..485  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:75037"  
/clone\_lib="Soares ovary tumor NBHOT"  
/sex="Female"  
/tissue\_type="ovarian tumor"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a

modified pGlylinker: Site.1 Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCATGTGAAGGCGGCGCCGCGGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo.

|            |       |       |      |       |
|------------|-------|-------|------|-------|
| BASE COUNT | 142 a | 103 c | 76 g | 164 f |
| ORIGIN     |       |       |      |       |

|                       |                 |                    |           |             |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match           | 11.8%;          | Score 475;         | DB 33;    | Length 485; |
| Best Local Similarity | 100.0%;         | Pred. No. 1.1e-78; |           |             |
| Matches 475;          | Conservative 0; | Mismatches 0;      | Indels 0; | Gaps 0;     |

|    |      |                                                                |      |
|----|------|----------------------------------------------------------------|------|
| QY | 1305 | agcctccagatgagatgagataatctatcttaccctcaactgacgtgaaacttctt       | 1364 |
| Db | 485  | AGCCTCAAGATGAGATGAGATATTTATTTTACCTCAGTGCACCTTGAAGATCTT         | 426  |
| QY | 1365 | cccatctccatctgttatctcgtggaacttaataatgaaactgaaactctgaccat       | 1422 |
| Db | 425  | CCCATCTCCATCTGTATATCTGGGAATTATTAAGAAACGAAACTAGCACCAAT          | 366  |
| QY | 1425 | taaaaaacaggcagctctaaagaaacacaggtcttctgttgagtgcgcacgaaaaact     | 1488 |
| Db | 365  | TAAAAACAGGAGCTCTAATGAAGCCACAGGTCTTATGTGTGATGCCGACCGAAAAACT     | 306  |
| QY | 1485 | aaaaataatgagcgctcttgagaaagatgtgcagtcattccatctgaactaataaagca    | 1544 |
| Db | 305  | AAAAATATGGCGCCTTGAGAAAGAGTGTGGAGTCATTCTCATTTGAATTATAAAAACA     | 246  |
| QY | 1545 | gcagagcttcaactaactgaggagcaaaagcaaaaagtatgatgatgtgtgagtaacttacc | 1604 |
| Db | 245  | GCAGGCTTCAAACTAGGGGGCAAAAGAAAAAGATGATAGTGGGACTTAAATTTATTC      | 186  |
| QY | 1605 | aagagttgtacaacctccctgagagagctataacttgcttggtctctgtgtcaactg      | 1664 |
| Db | 185  | AAGAGTTGTACAACTTCCGAGGGATCTATACTTCTTGTGTCTTTGTGTCAACATG        | 126  |
| QY | 1665 | aacaaatttatttgttagagggaacctaatgtgggtgcaaatgtaatgcaaaacttgagt   | 1724 |
| Db | 125  | AACAAATTTATTTGTAGGGGAACATTTTGGGGTGCAAATGCTAATGCAAACTTGAGT      | 66   |
| QY | 1725 | cacaaagaacatgtagaacaaacaaatgataaaacttgtatagtattgttggga         | 1779 |
| Db | 65   | CACAAAGACATGTAGAAAAACAAATGATAAATGTGATATGTATGTGTTGGGA           | 11   |

Search completed: January 20, 2000, 05:25:49  
Job time: 6362 sec

GenCore version 4.5  
Copyright (c) 1993 - 1998 Compugen Ltd.

OW protein - protein search, using sw model

Run on: January 19, 2000, 17:31:45 ; Search time 34.07 seconds

(Without alignments)  
264.183 Million cell updates/sec

Title: US-09-077-817-2

Sequence: 1 MAFVCLALGCLYFLISTTF.....LLLRKPNTYPMKIPFCDT 380

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A\_Geneseq\_36:\*

Word size: 0

Number of hits that pass the threshold: 188963

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID       | Description        |
|------------|--------|-------------|--------|----------|--------------------|
| 1          | 2104   | 100.0       | 380    | 1 W35295 | Human IL-13 bindin |
| 2          | 2104   | 100.0       | 380    | 1 W36613 | Human zcytor2 cyto |
| 3          | 2104   | 100.0       | 380    | 1 W41502 | Human cytokine/pep |
| 4          | 2104   | 100.0       | 380    | 1 W33603 | Homo sapiens HR-1  |
| 5          | 2104   | 100.0       | 380    | 1 W24972 | Human Interleukin- |
| 6          | 2104   | 100.0       | 380    | 1 W41520 | Human HR-1 recepto |
| 7          | 2078   | 98.8        | 380    | 1 W36614 | Human zcytor2 cyto |
| 8          | 1853   | 88.1        | 372    | 1 W36616 | Celebus macaque zc |
| 9          | 1753   | 83.3        | 359    | 1 W56260 | Construct containi |
| 10         | 1194.5 | 83.3        | 315    | 1 W56261 | Mature interleukin |
| 11         | 1194.5 | 56.8        | 383    | 1 W35294 | Murine IL-13 bindi |
| 12         | 456    | 21.7        | 157    | 1 W56252 | Interleukin-13 bin |
| 13         | 311.5  | 14.8        | 396    | 1 R22216 | Sequence of human  |
| 14         | 311.5  | 14.8        | 420    | 1 R22219 | Sequence of secret |
| 15         | 311.5  | 14.8        | 396    | 1 R22220 | Sequence of secret |
| 16         | 311.5  | 14.8        | 420    | 1 W82842 | Human Interleukin- |
| 17         | 310.5  | 14.8        | 421    | 1 R25064 | Human IL-5 recepto |
| 18         | 305.5  | 14.5        | 420    | 1 R22215 | Sequence of human  |
| 19         | 297    | 14.1        | 313    | 1 W21856 | Protein used in pr |
| 20         | 286    | 14.1        | 426    | 1 W09621 | Mouse Interleukin- |
| 21         | 295.5  | 14.0        | 427    | 1 W24973 | Human Interleukin- |
| 22         | 294.5  | 14.0        | 426    | 1 W09822 | Human Interleukin- |
| 23         | 292.5  | 13.9        | 1026   | 1 R70121 | IL5-R-GFP 130 fusi |
| 24         | 292    | 13.9        | 335    | 1 R25063 | Soluble human IL-5 |
| 25         | 292    | 13.9        | 335    | 1 R33699 | shIL-5R-alpha. Deo |
| 26         | 249.5  | 11.9        | 155    | 1 W56255 | Interleukin-13 bin |
| 27         | 248    | 11.7        | 398    | 1 R22212 | Sequence of Interl |
| 28         | 247    | 11.7        | 415    | 1 R22211 | Sequence of Interl |
| 29         | 247    | 11.7        | 415    | 1 R22217 | Sequence of Interl |
| 30         | 239    | 10.9        | 332    | 1 R22213 | Sequence of Interl |
| 31         | 239    | 10.9        | 315    | 1 R22214 | Sequence of Interl |
| 32         | 229    | 10.9        | 332    | 1 R22218 | Sequence of Interl |
| 33         | 220    | 10.5        | 369    | 1 R47148 | IL-2 receptor gamm |
| 34         | 219    | 10.4        | 347    | 1 R47149 | IL-2 receptor gamm |
| 35         | 209.5  | 10.0        | 369    | 1 R59094 | Murine IL-2R gamma |
| 36         | 209    | 9.9         | 482    | 1 W31646 | Human cytokine rec |
| 37         | 207    | 9.8         | 252    | 1 R47150 | IL-2 receptor gamm |
| 38         | 206    | 9.8         | 230    | 1 R47151 | IL-2 receptor gamm |
| 39         | 201.5  | 9.6         | 230    | 1 R82934 | Interleukin 4 comp |

|    |       |     |     |          |                    |
|----|-------|-----|-----|----------|--------------------|
| 40 | 195   | 9.3 | 878 | 1 R78608 | Murine IL-3 recept |
| 41 | 194   | 9.2 | 878 | 1 R92529 | Fas sequence from  |
| 42 | 185.5 | 8.8 | 154 | 1 W56257 | Interleukin-13 bin |
| 43 | 180.5 | 8.6 | 157 | 1 R20932 | Sequence of beta-c |
| 44 | 179   | 8.5 | 600 | 1 R78610 | Expression vector  |
| 45 | 179   | 8.5 | 596 | 1 R78616 | Expression vector  |

## ALIGNMENTS

|        |                                                                           |                                   |
|--------|---------------------------------------------------------------------------|-----------------------------------|
| R_SULT | W35295                                                                    | W35295 standard; Protein; 380 AA. |
| T      | W35295                                                                    |                                   |
| AJ     | W35295                                                                    |                                   |
| DT     | 27-MAR-1998                                                               | (first entry)                     |
| DE     | Human IL-13 binding chain of the IL-13 receptor.                          |                                   |
| EV     | Interleukin-13; IL-13; Interleukin-13 receptor binding chain; IL-13bc;    |                                   |
| KW     | mediator; IL-13 receptor binding inhibition; IgE-mediated condition;      |                                   |
| KW     | allergy; asthma; immune complex disorder.                                 |                                   |
| OR     | Homo sapiens.                                                             |                                   |
| FT     | Key                                                                       | Location/Qualifiers               |
| FT     | Peptide                                                                   | 1..25                             |
| FT     |                                                                           | /label="signal_sequence           |
| FT     | Protein                                                                   | /note="putative"                  |
| FT     |                                                                           | 26..380                           |
| FT     | Domain                                                                    | /label="mature_protein            |
| FT     |                                                                           | 26..341                           |
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| FT     |                                                                           | 342..362                          |
| FT     | Domain                                                                    | /label="transmembrane_domain      |
| FT     |                                                                           | 363..380                          |
| FT     | Domain                                                                    | /label="intracellular_domain      |
| PN     | W09731346-A1                                                              |                                   |
| PD     | 04-SEP-1997                                                               |                                   |
| PE     | 28-FEB-1997                                                               | U03124                            |
| PR     | 01-JAR-1996                                                               | US-609572                         |
| PA     | GENE J GENETICS-INST-INC.                                                 |                                   |
| PI     | Collins M, Donaldson D, Filtz L, Neben T, Whitters M,                     |                                   |
| PJ     | Wood C,                                                                   |                                   |
| DR     | WIT 97-448632/41.                                                         |                                   |
| DR     | W-OSB; T95214.                                                            |                                   |
| PT     | New nucleic acid encoding interleukin-13 receptor binding chain and       |                                   |
| PT     | transformed cells - proteins, antibodies and inhibitors, for              |                                   |
| PT     | treating immunoglobulin E-mediated diseases, e.g. Graves disease,         |                                   |
| PT     | and in diagnosis                                                          |                                   |
| ES     | Claim 11; Pages 34-35; 49pp; English.                                     |                                   |
| CC     | The present sequence represents the human interleukin-13 (IL-13) binding  |                                   |
| CC     | chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a  |                                   |
| CC     | mediator of the known biological activities of IL-13. Recombinant         |                                   |
| CC     | IL-13bc proteins, and antibodies raised against them, are used to         |                                   |
| CC     | inhibit the binding of IL-13 to its receptor. They are particularly used  |                                   |
| CC     | to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex |                                   |
| CC     | disorders, especially lupus, nephritis, thyroiditis and Grave's disease.  |                                   |
| CC     | They are also used to treat immune deficiency (particularly in            |                                   |
| CC     | haematopoietic progenitor cells), cancer etc., and to increase macrophage |                                   |
| CC     | activation, e.g. in vaccination. To potentiate IL-13 activity, a protein  |                                   |
| CC     | with such activity is combined with IL-13bc and the mixture applied,      |                                   |
| CC     | in vivo, to a cell expressing at least one chain of the IL-13 receptor    |                                   |
| CC     | other than IL-13bc. IL-13bc can also be used in diagnosis to detect       |                                   |
| CC     | expression of IL-13, its receptor or binding chain, and to raise specific |                                   |
| CC     | antibodies which may be useful for treating some tumours.                 |                                   |
| SC     | Sequence                                                                  | 370 AA.                           |

Query Match 100.0%; Score 2104; DB 1; Length 380;  
36% Local Similarity 100.0%; Pred. No. 8.1e-194;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLALGCLYFLISTTFGGSSSPTFEIKVNPDPDEFIVDPGYLGLYLQWQPPSLD 60  
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DE 1 MAFVCLALGCLYFLISTTFGGSSSPTFEIKVNPDPDEFIVDPGYLGLYLQWQPPSLD 60

QY 61 HEKECEVEYELKARNIGSEWTKITITKLNHYKGFDPNKGIEAKIHITLPMQCTNSSEVQ 120  
 DB 61 HEKECEVEYELKARNIGSEWTKITITKLNHYKGFDPNKGIEAKIHITLPMQCTNSSEVQ 120  
 QY 121 SSWAETTYWISPGIPEETKQVDMCYVNMQYLLCSMKRPGIGVLDNTNLFYWEGLDH 180  
 DB 121 SSWAETTYWISPGIPEETKQVDMCYVNMQYLLCSMKRPGIGVLDNTNLFYWEGLDH 180  
 QY 181 ALQCVYIKRAGDNIGCRPFYLEASDYKDFYICVNSSSEKPIRSSYFTFOLNIYKPLP 240  
 DB 181 ALQCVYIKRAGDNIGCRPFYLEASDYKDFYICVNSSSEKPIRSSYFTFOLNIYKPLP 240  
 QY 241 PVLFTFTRESSCEIKLWMSIPLGPIPARCFDYEIEIREDDTLVTATVENEYTLKTNE 300  
 DB 241 PVLFTFTRESSCEIKLWMSIPLGPIPARCFDYEIEIREDDTLVTATVENEYTLKTNE 300  
 QY 301 TROLCEVVRKSNVNYCSDGIMSEMSDKOCWEGEDLSKRTLLRFWLPFGFILLVIVTVG 360  
 DB 301 TROLCEVVRKSNVNYCSDGIMSEMSDKOCWEGEDLSKRTLLRFWLPFGFILLVIVTVG 360  
 QY 361 LLRKRPNTYPKMIPERFCDT 380  
 DB 361 LLRKRPNTYPKMIPERFCDT 380

RESULT 2  
 ID W36613 standard; Protein: 380 AA.  
 AC W36613;  
 DE Human Zcytor2 cytokine receptor protein.  
 DE Cytokine receptor; ligand binding; testicular cell; spermatogenesis;  
 KW Infertility; antagonist; contraceptive; diagnostic; therapeutic.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Domain 340..363  
 FT Domain /label= Transmembrane\_domain  
 FT Domain 364..380  
 FT Domain /label= Intracellular\_domain  
 FT Domain 25..339  
 FT Domain /label= ligand\_binding\_domain  
 PD WO9733913-A1.  
 PD 18-SEP-1997.  
 PF 12-MAR-1997; US-013345.  
 PR 13-MAR-1996; US-013345.  
 PA (ZYMO) ZYMOGENETICS INC.  
 PI Baumgartner JW, Farrah TM, Foster DC, Grant FU,  
 PI Ohara FJ;  
 DR MPI; 97-470820/43.  
 DR N-PSDB; T96782.  
 PT New nucleic acid encoding testis-specific cytokine receptor - useful  
 PT for identification of ligands or antagonists, potentially for use as  
 PT male contraceptives or for infertility treatment  
 PS Claim 2; Page 47-48; 79pp; English.  
 CC This sequence represents a novel ligand-binding receptor, Zcytor2,  
 CC which shares homology with cytokine receptors and was isolated from human  
 CC placental polyA+ RNA. The resulting polypeptide is a receptor for  
 CC cytokines (particularly interleukin-13) and is expressed on the surface  
 CC of testicular cells, probably being involved in spermatogenesis. It can  
 CC be used to detect ligands that promote proliferation and/or  
 CC differentiation of such cells in cultures and may also be used to treat  
 CC infertility. Antagonists of this receptor may be used to characterise  
 CC ligand-receptor interactions and as male-specific contraceptives. By  
 CC blocking the action of IL-13, receptor antagonists and ligand-binding  
 CC this receptor can also be used to modulate immune function, e.g. in  
 CC allergy and asthma, as a diagnostic to determine circulating levels of  
 CC ligand and also to isolate and purify ligands. Antibodies can be used to  
 CC assay circulating receptor (an abnormal level may be indicative of  
 CC disease such as cancer), for labelling cells that express the receptor,  
 CC and therapeutically as antagonist.  
 SO Sequence 380 AA.

Query Match 100.0%; Score 2104; DB 1; Length 380;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-194;  
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVVCAIGLTYFLISTTGGCTSSSDTEKVNPPDFFYVDGYYGYYLQWQPLSLD 60  
 DB 1 MAVVCAIGLTYFLISTTGGCTSSSDTEKVNPPDFFYVDGYYGYYLQWQPLSLD 60  
 QY 61 HEKECEVEYELKARNIGSEWTKITITKLNHYKGFDPNKGIEAKIHITLPMQCTNSSEVQ 120  
 DB 61 HEKECEVEYELKARNIGSEWTKITITKLNHYKGFDPNKGIEAKIHITLPMQCTNSSEVQ 120  
 QY 121 SSWAETTYWISPGIPEETKQVDMCYVNMQYLLCSMKRPGIGVLDNTNLFYWEGLDH 180  
 DB 121 SSWAETTYWISPGIPEETKQVDMCYVNMQYLLCSMKRPGIGVLDNTNLFYWEGLDH 180  
 QY 181 ALQCVYIKRAGDNIGCRPFYLEASDYKDFYICVNSSSEKPIRSSYFTFOLNIYKPLP 240  
 DB 181 ALQCVYIKRAGDNIGCRPFYLEASDYKDFYICVNSSSEKPIRSSYFTFOLNIYKPLP 240  
 QY 241 PVLFTFTRESSCEIKLWMSIPLGPIPARCFDYEIEIREDDTLVTATVENEYTLKTNE 300  
 DB 241 PVLFTFTRESSCEIKLWMSIPLGPIPARCFDYEIEIREDDTLVTATVENEYTLKTNE 300  
 QY 301 TROLCEVVRKSNVNYCSDGIMSEMSDKOCWEGEDLSKRTLLRFWLPFGFILLVIVTVG 360  
 DB 301 TROLCEVVRKSNVNYCSDGIMSEMSDKOCWEGEDLSKRTLLRFWLPFGFILLVIVTVG 360  
 QY 361 LLRKRPNTYPKMIPERFCDT 380  
 DB 361 LLRKRPNTYPKMIPERFCDT 380

RESULT 3  
 ID W41502 standard; Protein: 380 AA.  
 AC W41502;  
 DE 08-JUN-1998 (first entry)  
 DE Human cytokine/peptide receptor, HR-1 receptor.  
 KW HR-1 receptor; cytokine receptor; peptide hormone receptor; human;  
 KW infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;  
 KW neutropenia; therapy.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Peptide 1..21  
 FT Protein /label= Sig\_peptide  
 FT Protein 22..380  
 FT Protein /label= Mat\_protein  
 FT Protein /note= "Claim 14"  
 PD EP-812913-A2.  
 PD 17-DEC-1997.  
 PF 04-JUN-1997; 303815.  
 PR 12-JUN-1996; US-017343.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (SMK) SMITHKLINE BEECHAM CORP.  
 PI Appelbaum ER, Hu J;  
 DR MPI; 98-034974/04.  
 DR N-PSDB; V04075.  
 PT Human cytokine/peptide hormone receptor, HR-1 receptor - useful to  
 PT increase resistance to infections in individuals with trauma and/or  
 PT burns  
 PS Claim 13; Page 27-28; 34pp; English.  
 CC This protein comprises a novel human cytokine/peptide hormone  
 CC receptor, designated HR-1 receptor. The amino acid sequence  
 CC was deduced from a cDNA clone (see V04075) isolated from a human  
 CC testis cDNA library. It shows 27% amino acid identity and 52%  
 CC similarity with the human interleukin-5 receptor. Also claimed are  
 CC polynucleotides encoding HR-1 receptor, vector and host cells, an  
 CC agonist to the polypeptide, antibody against the polypeptide, an  
 CC antagonist that inhibits the activity of the polypeptide, a process  
 CC for diagnosing a disease, or a susceptibility to disease, related  
 CC to expression of HR-1 receptor, and a method for identifying  
 CC compounds that activate or inhibit the HR-1 receptor. HR-1

receptor protein and polynucleotides can be used for research, biological, diagnosis and (gene) therapy applications, e.g. to increase resistance to infections in individuals with trauma and/or burns, and to prevent, ameliorate, treat, diagnose and/or determine predisposition to asthma, allergic disorders or disorders of haematopoiesis induced by AIDS, aplastic anaemia, congenital or cyclic neutropenia or as a consequence of cytotoxic therapy of cancer, lymphoma, leukaemia and/or bone marrow transplantation.

Sequence 380 AA:

Query Match 100.0%; Score 2104; DB 1; Length 380;  
Best Local Similarity 100.0%; Pred. No. 8.1e-194;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIIGLTYFLISTFTGCTSSDTEIKVNPPOFEIYDPGLYLYLQMPPLSLD 60  
DB 1 MAFVCLAIIGLTYFLISTFTGCTSSDTEIKVNPPOFEIYDPGLYLYLQMPPLSLD 60  
QY 61 HFKECTVEYEELKYNISSETWKTITTKNLHYKDGFDLNKGIEAKIHLLPQCNGSEVQ 120  
DB 61 HFKECTVEYEELKYNISSETWKTITTKNLHYKDGFDLNKGIEAKIHLLPQCNGSEVQ 120  
QY 121 SSMAETTYWISPGIPEKTVQDMDCVYYNMQYLCSMKRPGIGVLLDTNVLNLFYWEGLDH 180  
DB 121 SSMAETTYWISPGIPEKTVQDMDCVYYNMQYLCSMKRPGIGVLLDTNVLNLFYWEGLDH 180  
QY 181 ALQCVDIKADGNIKGRFPLEASDYKDFIYICVNGSSENNPINSYTFPOLNIVKRLP 240  
DB 181 ALQCVDIKADGNIKGRFPLEASDYKDFIYICVNGSSENNPINSYTFPOLNIVKRLP 240  
QY 241 PVLITFTRESSCEIKLWKSIPLGPIPARCFDEYEIRDDTTLTAAYENETYLKLTNE 300  
DB 241 PVLITFTRESSCEIKLWKSIPLGPIPARCFDEYEIRDDTTLTAAYENETYLKLTNE 300  
QY 301 TROLCEYVRSKVNITYCSDDGIMSEMSDKQCEGDELKSKTLLRFWLPFGFILLIVIFVTG 360  
DB 301 TROLCEYVRSKVNITYCSDDGIMSEMSDKQCEGDELKSKTLLRFWLPFGFILLIVIFVTG 360  
QY 361 LLRKPNTPYPMIPEFCDT 380  
DB 361 LLRKPNTPYPMIPEFCDT 380

#### RESULT 4

ID W33603 standard; protein; 380 AA.

AC W33603;  
DT 08-JUN-1998 (first entry)  
DE Homo sapiens HR-1 receptor.  
KW Cytokine; hormone receptor; AIDS; acquired immune deficiency;  
KW syndrome; aplastic anaemia; neutropenia; cancer treatment;  
KW infection resistance; diagnosis; tumours; HR-1 receptor;  
KW asthma; allergic; haematopoietic disorder.  
OS Homo sapiens.  
FH key location/Qualifiers  
FT Peptide 1.21  
FT /note- "signal peptide"  
PN W09747742-A1.  
PD 18-DEC-1997.  
PF 09-JUL-1996; U11459.  
PR 12-JUN-1996; WO-010262.  
PR 12-JUN-1996; US-017843.  
PA (HUMA-) HUMAN GENE SCI INC.  
PA (SMK-) SMITHKLINE BEECHAM CORP.  
PI Appelbaum ER, Hu J;  
PI WPI; 98-052309/05.  
DR N-PSDB; V02295.  
PT DNA encoding human cytokine-peptide hormone receptor - useful for  
PT treating preventing or diagnosing, e.g. lowered resistance to  
PT infection, asthma, allergy, or haematopoietic disease  
PS Claim 15; Fig 1; 75pp; English.  
CC The sequence is that of the human cytokine/peptide hormone receptor

(HR-1 receptor). This, or its activators or agonists, can be used to treat, prevent or diagnose predisposition to lowered resistance to infection, asthma, allergic or haematopoietic disorders, e.g. where induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia, neutropenia or cytotoxic treatments for cancer. Antagonists of the receptor, e.g. antibodies or fragments of it may be used to treat conditions associated with overexpression of the HR-1 receptor, e.g. those listed above. Antibodies may also be used to assay levels of HR-1 receptor overexpression of which may be diagnostic of tumours, by usual immunassays; to isolate and identify HR-1 receptor-expressing cells; or for affinity purification of the HR-1 receptor.

Sequence 380 AA:

Query Match 100.0%; Score 2104; DB 1; Length 380;  
Best Local Similarity 100.0%; Pred. No. 8.1e-194;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIIGLTYFLISTFTGCTSSDTEIKVNPPOFEIYDPGLYLYLQMPPLSLD 60  
DB 1 MAFVCLAIIGLTYFLISTFTGCTSSDTEIKVNPPOFEIYDPGLYLYLQMPPLSLD 60  
QY 61 HFKECTVEYEELKYNISSETWKTITTKNLHYKDGFDLNKGIEAKIHLLPQCNGSEVQ 120  
DB 61 HFKECTVEYEELKYNISSETWKTITTKNLHYKDGFDLNKGIEAKIHLLPQCNGSEVQ 120  
QY 121 SSMAETTYWISPGIPEKTVQDMDCVYYNMQYLCSMKRPGIGVLLDTNVLNLFYWEGLDH 180  
DB 121 SSMAETTYWISPGIPEKTVQDMDCVYYNMQYLCSMKRPGIGVLLDTNVLNLFYWEGLDH 180  
QY 181 ALQCVDIKADGNIKGRFPLEASDYKDFIYICVNGSSENNPINSYTFPOLNIVKRLP 240  
DB 181 ALQCVDIKADGNIKGRFPLEASDYKDFIYICVNGSSENNPINSYTFPOLNIVKRLP 240  
QY 241 PVLITFTRESSCEIKLWKSIPLGPIPARCFDEYEIRDDTTLTAAYENETYLKLTNE 300  
DB 241 PVLITFTRESSCEIKLWKSIPLGPIPARCFDEYEIRDDTTLTAAYENETYLKLTNE 300  
QY 301 TROLCEYVRSKVNITYCSDDGIMSEMSDKQCEGDELKSKTLLRFWLPFGFILLIVIFVTG 360  
DB 301 TROLCEYVRSKVNITYCSDDGIMSEMSDKQCEGDELKSKTLLRFWLPFGFILLIVIFVTG 360  
QY 361 LLRKPNTPYPMIPEFCDT 380  
DB 361 LLRKPNTPYPMIPEFCDT 380

#### RESULT 5

ID W24972 standard; protein; 380 AA.

AC W24972;  
DT 22-JUN-1996 (first entry)  
DE Human interleukin-13 beta receptor.  
KW Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.  
OS Homo sapiens.  
FH key location/Qualifiers  
FT Peptide 1.21  
FT /note- "signal peptide"  
PN W09723925-A1.  
PD 12-JUN-1997.  
PF 07-NOV-1996; F01756.  
PR 16-DEC-1995; FR-014424.  
PA (SMK-) SANOFI SA.  
PI Leprieu D, Ferrara P, Laurent P, Vita N;  
PI PI; 97-319773/29.  
DR N-PSDB; T85826, T86464.  
PT New purified human interleukin-13 receptors - and related nucleic  
PT acids, useful for diagnosis and treatment of inflammation, allergy,  
PT etc  
PS Claim 1; Figure 2a; 83pp; French  
CC This sequence represents interleukin-13 (IL-13) beta receptor. The  
CC invention relates to new purified peptides comprising 380 or 427 amino  
CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380  
CC and 427 aa proteins are designated IL-13R beta and alpha respectively.  
CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low  
CC affinity, but acquires high affinity when associated with the IL-4

receptor. Nucleic acids encoding IL-13R beta and alpha are used as diagnostic probes to identify aberrant synthesis or genetic anomalies such as loss of heterozygosity and rearrangements, or chromosomal anomalies. They are also used for production of recombinant IL-13R beta and alpha which can be used as IL-13 antagonists, specifically to regulate IL-13-induced responses for treatment of inflammation and allergy. IL-13 receptors are also useful as antisense molecules for gene therapy (blocking synthesis of IL-13R). Antibodies are used (in standard immunoassays) to diagnose diseases associated with abnormal expression of IL-13 receptors; when coupled to a toxin also for treatment of overproduction of IL-13R. Cells that express IL-13R at the surface are used to identify ligands and modulators of IL-13R. Note: IL-13R beta is encoded by the nucleic acid sequence shown in Figure 2a in the CC specification (T86464), which is not the same as that shown in the CC sequence listing (T85828).

Query Match 100.0%; Score 2104; DB 1; Length 380;  
Best Local Similarity 100.0%; Pred. No. 8, 1e-194;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAVVCAIGCLYFLSTFGCTSSDTEIKVNPPODFEIVDGYGLYLQWQPLSLD 60  
1 MAVVCAIGCLYFLSTFGCTSSDTEIKVNPPODFEIVDGYGLYLQWQPLSLD 60  
61 HFECEVEYELKRNIGSETWKTITRNKLYKDGFDLNGIEAKIHTLLPWQCTNSEVQ 120  
61 HFECEVEYELKRNIGSETWKTITRNKLYKDGFDLNGIEAKIHTLLPWQCTNSEVQ 120  
121 SSAEETTWISPGIPETKYQDMDCVYNNQYLLCSMKRPGIGVLDITNNLYFWYEGLDH 180  
121 SSAEETTWISPGIPETKYQDMDCVYNNQYLLCSMKRPGIGVLDITNNLYFWYEGLDH 180  
181 ALQCVYIRADGONICRPFYLEASDKDFYICVNGSSEKPRSSYFTFOLNIVKPLP 240  
181 ALQCVYIRADGONICRPFYLEASDKDFYICVNGSSEKPRSSYFTFOLNIVKPLP 240  
241 PVLFTFTRESSCEIKLWKSIPILGPIPARCFDEIEIREDDTLVTAVENETYLKTNE 300  
241 PVLFTFTRESSCEIKLWKSIPILGPIPARCFDEIEIREDDTLVTAVENETYLKTNE 300  
301 TROLCFVRSKVNIVYCSDDGIMSEMSDKOCWGEDLSKRTLLRFWLPFGIILLVIVTVG 360  
301 TROLCFVRSKVNIVYCSDDGIMSEMSDKOCWGEDLSKRTLLRFWLPFGIILLVIVTVG 360  
361 LLRKRPNTYPKMIPEFFCDT 380  
361 LLRKRPNTYPKMIPEFFCDT 380

RESULT 6  
W41520  
ID W41520 standard; Protein: 380 AA.  
AC W41520:  
DT 22-JUN-1998 (first entry)  
DE Human HR-1 receptor.  
KW HR-1 receptor; human; cytokine; infection; asthma; allergy;  
KW haematopoietic disorder; tumour; therapy; diagnosis.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..21  
FT Protein /label= Sfg\_peptide  
FT Protein /label= Mat\_protein  
PD WO9747741-A1.  
PD 18-DEC-1997.  
PE 12-JUN-1996; U10262.  
PR 12-JUN-1996; WO-010262.  
PA (HUMA-) HUMAN GENOME SCI. INC.  
PA (SMK-) SMITHKLINE BEECHAM CORP.  
PI Appelbaum ER, Hu J;  
DR WPI: 98-052308/05.

N-PSDB; V04131.  
Nucleic acid sequence encoding human cytokine peptide hormone receptor - useful to treat, prevent or diagnose, e.g. lowered resistance to infection, asthma, allergy or haematopoietic disease  
PS Claim 13; Page 62-64; 76pp; English.  
This protein comprises a novel human cytokine/peptide hormone receptor, designated the HR-1 receptor, that shows 27% identity and 52% similarity to the interleukin-5 receptor. Its amino acid sequence was deduced from a cDNA clone (see V04131) obtained from a human testis library. Recombinant HR-1 receptor can be expressed in claimed host cells, and used in a claimed method for identifying compounds which bind to, and activate or inhibit, it. HR-1 receptor activators and agonists can be used to treat, prevent or CC diagnose predisposition to lowered resistance to infection, asthma, CC allergic or haematopoietic disorders, e.g. where induced by AIDS, CC aplastic anaemia, neutropenia or cytotoxic treatments for cancer. CC HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can be used to treat conditions associated with HR-1 receptor overexpression. The antibodies can also be used to determine HR-1 receptor levels, since overexpression may be diagnostic of tumours.

Query Match 100.0%; Score 2104; DB 1; Length 380;  
Best Local Similarity 100.0%; Pred. No. 8, 1e-194;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAVVCAIGCLYFLSTFGCTSSDTEIKVNPPODFEIVDGYGLYLQWQPLSLD 60  
1 MAVVCAIGCLYFLSTFGCTSSDTEIKVNPPODFEIVDGYGLYLQWQPLSLD 60  
61 HFECEVEYELKRNIGSETWKTITRNKLYKDGFDLNGIEAKIHTLLPWQCTNSEVQ 120  
61 HFECEVEYELKRNIGSETWKTITRNKLYKDGFDLNGIEAKIHTLLPWQCTNSEVQ 120  
121 SSAEETTWISPGIPETKYQDMDCVYNNQYLLCSMKRPGIGVLDITNNLYFWYEGLDH 180  
121 SSAEETTWISPGIPETKYQDMDCVYNNQYLLCSMKRPGIGVLDITNNLYFWYEGLDH 180  
181 ALQCVYIRADGONICRPFYLEASDKDFYICVNGSSEKPRSSYFTFOLNIVKPLP 240  
181 ALQCVYIRADGONICRPFYLEASDKDFYICVNGSSEKPRSSYFTFOLNIVKPLP 240  
241 PVLFTFTRESSCEIKLWKSIPILGPIPARCFDEIEIREDDTLVTAVENETYLKTNE 300  
241 PVLFTFTRESSCEIKLWKSIPILGPIPARCFDEIEIREDDTLVTAVENETYLKTNE 300  
301 TROLCFVRSKVNIVYCSDDGIMSEMSDKOCWGEDLSKRTLLRFWLPFGIILLVIVTVG 360  
301 TROLCFVRSKVNIVYCSDDGIMSEMSDKOCWGEDLSKRTLLRFWLPFGIILLVIVTVG 360  
361 LLRKRPNTYPKMIPEFFCDT 380  
361 LLRKRPNTYPKMIPEFFCDT 380

RESULT 7  
W36614  
ID W36614 standard; Protein: 380 AA.  
AC W36614:  
DT 30-MAR-1998 (first entry)  
DE Human zcyto2 cytokine receptor protein.  
KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;  
KW infertility; antagonist; contraceptive; diagnostic; therapeutic.  
OS Homo sapiens.  
FH WO9733913-A1.  
PD 18-SEP-1997.  
PE 12-MAR-1997; U04043.  
PR 13-MAR-1996; US-013345.  
PA (ZYMO-) ZYMOGENETICS INC.  
PA Baumgartner JW, Fairrah TM, Foster DC, Grant FJ,  
PI Ohara PJ;  
DR WPI: 97-470820/43.

DR N-PSDB; T96783.  
 PT New nucleic acid encoding testis-specific cytokine receptor - useful  
 PT for identification of ligands or antagonists, potentially for use as  
 PT male contraceptives or for infertility treatment  
 PS Claim 1: Page 51-53; 79pp: English.  
 CC This sequence represents a novel ligand-binding receptor, Zcytor2, which  
 CC shares homology with cytokine receptors and was isolated from a human  
 CC testis cDNA library. The resulting polypeptide is a receptor for  
 CC cytokines (particularly interleukin-13) and is expressed on the surface  
 CC of testicular cells, probably being involved in spermatogenesis. It can  
 CC be used to detect ligands that promote proliferation and/or  
 CC differentiation of such cells in cultures and may also be used to treat  
 CC infertility. Antagonists of this receptor may be used to characterise  
 CC ligand-receptor interactions and as male-specific contraceptives. By  
 CC blocking the action of IL-13, receptor antagonists and ligand-binding  
 CC this receptor can also be used to modulate immune function, e.g. in  
 CC allergy and asthma, as a diagnostic to determine circulating levels of  
 CC ligand and also to isolate and purify ligands. Antibodies can be used to  
 CC assay circulating receptor (an abnormal level may be indicative of  
 CC disease such as cancer), for labelling cells that express the receptor,  
 CC and therapeutically as antagonist.  
 SO Sequence 380 AA.

Query Match 98.8%; Score 2078; DB 1; Length 380;  
 Best Local Similarity 99.2%; Pred. No. 2.5e-191;  
 Matches 377; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLSTTGGCTSSDTEIKVNPDPFEYDPEYLGILYQWPPSLD 60  
 DB 1 MAFVCLAIGCLYTLSTTGGCTSSDTEIKVNPDPFEYDPEYLGILYQWPPSLD 60  
 QY 61 HFEKCTVEYELKRNISESEMTKTIITKLNHYKQGFENKIGIAKIHLLPMQCNSEVQ 120  
 DB 61 HFEKCTVEYELKRNISESEMTKTIITKLNHYKQGFENKIGIAKIHLLPMQCNSEVQ 120  
 QY 121 SSWAETTWISPOGIPETKVQDMDCVYNNQYLLCSMKPGIGVLLDNNYLFYEGIDL 180  
 DB 121 SSWAETTWISPOGIPETKVQDMDCVYNNQYLLCSMKPGIGVLLDNNYLFYEGIDL 180  
 QY 181 ALQCVDIKADGONIGRFPYLEASDKDFYICVNGSSENKPISSFTFOLQNIIVPLP 240  
 DB 181 ALQCVDIKADGONIGRFPYLEASDKDFYICVNGSSENKPISSFTFOLQNIIVPLP 240  
 QY 241 PVLTFRESSECEIKLWSPILGIPARCFDYEIEIEDDTLTVATVENTYTLKTNE 300  
 DB 241 PVLTFRESSECEIKLWSPILGIPARCFDYEIEIEDDTLTVATVENTYTLKTNE 300  
 QY 301 TROLCEVRSKVNIVYCSDDGIMWSEMSDKQCEGDELRSKTLRFLWLPFGFILLIVFVVG 360  
 DB 301 TROLCEVRSKVNIVYCSDDGIMWSEMSDKQCEGDELRSKTLRFLWLPFGFILLIVFVVG 360  
 QY 361 LLRKRPNTYPKMIPFECDT 380  
 DB 361 LLRKRPNTYPKMIPFECDT 380

RESULT 8  
 W36616  
 ID W36616 standard; Protein; 372 AA.  
 AC W36616;  
 DT 30-MAR-1998 (first entry)  
 DE Celebus macaque Zcytor2 protein.  
 KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;  
 OS Infertility; antagonist; contraceptive; diagnostic; therapeutic.  
 OS Macaque sp.  
 FH Key  
 FT Location/Qualifiers  
 FT 1.372  
 FT /label= Zcytor2  
 FT /note= "partial protein sequence"

PD MO9733913-AL.  
 PD 18-SEP-1997.  
 PE 12-MAR-1997; U04043.

PR 13-MAR-1996; US-013345.  
 PT (Zymo) ZYM-GENETICS INC.  
 PT Bounded; JM, Farrah TM, Foster DC, Grant FT,  
 PT Chera RJ.  
 PS SPT; 97-470820/43.  
 DR N-PSDB; T96784.  
 PT New nucleic acid encoding testis-specific cytokine receptor - useful  
 PT for identification of ligands or antagonists, potentially for use as  
 PT male contraceptives or for infertility treatment  
 PS Example 4: Page 56-57; 79pp: English.  
 CC This sequence represents a novel ligand-binding receptor, Zcytor2,  
 CC which shares homology with cytokine receptors and is isolated from  
 CC testis tissue obtained from a Celebus macaque. The resulting polypeptide  
 CC is a receptor for cytokines (particularly interleukin-13) and is  
 CC expressed on the surface of testicular cells, probably being involved in  
 CC spermatogenesis. It can be used to detect ligands promoting proliferation  
 CC and/or differentiation of such cells in cultures and may also be used to  
 CC treat infertility. Antagonists of this receptor may be used to  
 CC characterise ligand-receptor interactions and as male-specific  
 CC contraceptives. By blocking the action of IL-13, receptor antagonists and  
 CC ligand-binding this receptor can also be used to modulate immune  
 CC function, e.g. in allergy and asthma, as a diagnostic to determine  
 CC circulating levels of ligand and also to isolate and purify ligands.  
 CC Antibodies can be used to assay circulating receptor (an abnormal level  
 CC may be indicative of disease such as cancer), for labelling cells that  
 CC express the receptor, and therapeutically as antagonist.  
 SO Sequence 372 AA.

Query Match 88.1%; Score 1853; DB 1; Length 372;  
 Best Local Similarity 92.2%; Pred. No. 9.2e-170;  
 Matches 343; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLSTTGGCTSSDTEIKVNPDPFEYDPEYLGILYQWPPSLD 60  
 DB 1 MAFVCLAIGCLYTLSTTGGCTSSDTEIKVNPDPFEYDPEYLGILYQWPPSLD 60  
 QY 61 HFEKCTVEYELKRNISESEMTKTIITKLNHYKQGFENKIGIAKIHLLPMQCNSEVQ 120  
 DB 61 HFEKCTVEYELKRNISESEMTKTIITKLNHYKQGFENKIGIAKIHLLPMQCNSEVQ 120  
 QY 121 SSWAETTWISPOGIPETKVQDMDCVYNNQYLLCSMKPGIGVLLDNNYLFYEGIDL 180  
 DB 121 SSWAETTWISPOGIPETKVQDMDCVYNNQYLLCSMKPGIGVLLDNNYLFYEGIDL 180  
 QY 181 ALQCVDIKADGONIGRFPYLEASDKDFYICVNGSSENKPISSFTFOLQNIIVPLP 240  
 DB 181 ALQCVDIKADGONIGRFPYLEASDKDFYICVNGSSENKPISSFTFOLQNIIVPLP 240  
 QY 241 PVLTFRESSECEIKLWSPILGIPARCFDYEIEIEDDTLTVATVENTYTLKTNE 300  
 DB 241 PVLTFRESSECEIKLWSPILGIPARCFDYEIEIEDDTLTVATVENTYTLKTNE 300  
 QY 301 TROLCEVRSKVNIVYCSDDGIMWSEMSDKQCEGDELRSKTLRFLWLPFGFILLIVFVVG 360  
 DB 301 TROLCEVRSKVNIVYCSDDGIMWSEMSDKQCEGDELRSKTLRFLWLPFGFILLIVFVVG 360  
 QY 361 LLRKRPNTYPKM 372  
 DB 361 LLRKRPNTYPKM 372

RESULT 9  
 W56260  
 ID W56260 standard; Protein; 359 AA.  
 AC W56260;  
 DT 16-SEP-1993 (first entry)  
 DE Construct containing mature interleukin-13 binding protein.  
 KW Therapeutic; IL-13 mediated condition; allergy; asthma; diagnosis;  
 OS Homo sapiens.  
 OS Homo sapiens.  
 OS MO9810539-AL.  
 PE 19-MAR-1993.

PF 10-SEP-1997; AU0591.  
 PR 27-FEB-1997; AU-005374.  
 PR 10-SEP-1996; AU-002262.  
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
 PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;  
 DR WPI: 98-207062/18.  
 DR N-PSDB: V22702.  
 PT New isolated interleukin-13 binding protein - used to develop  
 PT products for therapy e.g. for allergic conditions such as asthma or  
 PT for diagnosis or detection  
 PS Example 14: Page 52-53: 69pp: English.  
 CC The IL-13 binding protein and related therapeutic molecules can be used  
 CC in the antagonism of at least one IL-13 activity. They can be used for  
 CC treating IL-13 mediated conditions such as certain allergic conditions  
 CC such as asthma or to inactivate locally administered IL-13 after IL-13  
 CC treatment. The products can also be used as diagnostic agents, e.g. for  
 CC detecting autoimmune diseases. The antibodies can also be used for  
 CC immunotherapy and may also be used as a diagnostic tool.  
 SO Sequence 359 AA;

Query Match 83.3%; Score 1753; DB 1; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 3, 4e-160;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EIKVNPDDFVDPGIGLYLQWOPPLSDHFEKCTVEYELKRNIGSETWKTITKN 88  
 DB 45 EIKVNPDDFVDPGIGLYLQWOPPLSDHFEKCTVEYELKRNIGSETWKTITKN 104  
 QY 89 LHYKDFDLNKGIEAKIHTLLPMQCTNGSEVOSSMAETTWISPGIPETKVQDMDCVY 148  
 DB 105 LHYKDFDLNKGIEAKIHTLLPMQCTNGSEVOSSMAETTWISPGIPETKVQDMDCVY 164  
 QY 149 NMOTLLCSMRPGIGVLDNTNLFYWEGLDHALQCVDIKADGONIGCRFPYLEASDYK 208  
 DB 165 NMOTLLCSMRPGIGVLDNTNLFYWEGLDHALQCVDIKADGONIGCRFPYLEASDYK 224  
 QY 209 DEYICVNGSSSEKPIRSSYTFPOLNIVKPLPVYILTFRESCEIKLWSPILGPIPAR 268  
 DB 225 DEYICVNGSSSEKPIRSSYTFPOLNIVKPLPVYILTFRESCEIKLWSPILGPIPAR 284  
 QY 269 CFDEYEIREDDTLVATAVENETYLKTTNETRQLCFVRSKNIYICSDDGIMSEMSDK 328  
 DB 285 CFDEYEIREDDTLVATAVENETYLKTTNETRQLCFVRSKNIYICSDDGIMSEMSDK 344  
 QY 329 QCWEGEDLSKTLIR 343  
 DB 345 QCWEGEDLSKTLIR 359

## RESULT 10

ID W56261 standard; Protein; 315 AA.  
 AC W56261;  
 DT 16-SEP-1998 (first entry)  
 DE Mature interleukin-13 binding protein.  
 KW Therapeutic; IL-13 mediated condition; allergy; asthma; diagnosis;  
 KW autoimmune disease; antibody; immunotherapy.  
 OS Homo sapiens.  
 PN MO9810638-A1.  
 PD 19-MAR-1998.  
 PF 10-SEP-1997; AU0591.  
 PR 27-FEB-1997; AU-005374.  
 PR 10-SEP-1996; AU-002262.  
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
 PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;  
 DR WPI: 98-207062/18.  
 DR N-PSDB: V22702.  
 PT New isolated interleukin-13 binding protein - used to develop  
 PT products for therapy e.g. for allergic conditions such as asthma or  
 PT for diagnosis or detection  
 PS Disclosure; Page 55-56; 69pp; English.  
 CC The IL-13 binding protein and related therapeutic molecules can be used

CC in the antagonism of at least one IL-13 activity. They can be used for  
 CC treating IL-13 mediated conditions such as certain allergic conditions  
 CC such as asthma or to inactivate locally administered IL-13 after IL-13  
 CC treatment. The products can also be used as diagnostic agents, e.g. for  
 CC detecting autoimmune diseases. The antibodies can also be used for  
 CC immunotherapy and may also be used as a diagnostic tool.  
 SO Sequence 315 AA;

Query Match 83.3%; Score 1753; DB 1; Length 315;  
 Best Local Similarity 100.0%; Pred. No. 2, 8e-160;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EIKVNPDDFVDPGIGLYLQWOPPLSDHFEKCTVEYELKRNIGSETWKTITKN 88  
 DB 1 EIKVNPDDFVDPGIGLYLQWOPPLSDHFEKCTVEYELKRNIGSETWKTITKN 60  
 QY 89 LHYKDFDLNKGIEAKIHTLLPMQCTNGSEVOSSMAETTWISPGIPETKVQDMDCVY 148  
 DB 61 LHYKDFDLNKGIEAKIHTLLPMQCTNGSEVOSSMAETTWISPGIPETKVQDMDCVY 120  
 QY 149 NMOTLLCSMRPGIGVLDNTNLFYWEGLDHALQCVDIKADGONIGCRFPYLEASDYK 208  
 DB 121 NMOTLLCSMRPGIGVLDNTNLFYWEGLDHALQCVDIKADGONIGCRFPYLEASDYK 180  
 QY 209 DEYICVNGSSSEKPIRSSYTFPOLNIVKPLPVYILTFRESCEIKLWSPILGPIPAR 268  
 DB 181 DEYICVNGSSSEKPIRSSYTFPOLNIVKPLPVYILTFRESCEIKLWSPILGPIPAR 240  
 QY 269 CFDEYEIREDDTLVATAVENETYLKTTNETRQLCFVRSKNIYICSDDGIMSEMSDK 328  
 DB 241 CFDEYEIREDDTLVATAVENETYLKTTNETRQLCFVRSKNIYICSDDGIMSEMSDK 300  
 QY 329 QCWEGEDLSKTLIR 343  
 DB 301 QCWEGEDLSKTLIR 315

## RESULT 11

ID W35294 standard; Protein; 383 AA.  
 AC W35294;  
 DT 27-MAR-1998 (first entry)  
 DE Murine IL-13 binding chain of the IL-13 receptor.  
 KW Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;  
 KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;  
 KW allergy; asthma; immune complex disorder.  
 OS Mus sp.  
 PN M09731946-A1.  
 PD 04-SEP-1997.  
 PF 28-FEB-1997; U03124.  
 PR 01-MAR-1996; US-609572.  
 PA (GENY) GENETICS INST INC.  
 PI Collins M, Donaldson D, Filtz L, Neben T, Whitters M,  
 DR WPI: 97-448632/41.  
 DR N-PSDB: T75213.  
 PT New nucleic acid encoding interleukin-13 receptor binding chain and  
 PT transformed cells - proteins, antibodies and inhibitors, for  
 PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,  
 and in diagnosis



PS Claim 11: Pages 30-31: 49pp; English.  
 CC The present sequence represents the murine interleukin-13 (IL-13) binding  
 CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a  
 CC mediator of the known biological activities of IL-13. Recombinant  
 CC IL-13bc proteins, and antibodies raised against them, are used to  
 CC inhibit the binding of IL-13 to its receptor. They are particularly used  
 CC to treat IIS-mediated conditions, e.g. allergy, asthma and immune complex  
 CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.  
 CC They are also used to treat immune deficiency (particularly in  
 CC hematopoietic progenitor cells), cancer etc., and to increase macrophage  
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein  
 CC with such activity is combined with IL-13bc and the mixture applied,  
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor  
 CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect  
 CC expression of IL-13, its receptor or binding chain, and to raise specific  
 CC antibodies which may be useful for treating some tumours.  
 SQ Sequence 383 AA;

Query Match 56.8%; Score 1194.5; DB 1; Length 383;  
 Best Local Similarity 58.9%; Pred. No. 1.3e-106;  
 Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

QY 1 MAFVCLAIGCLYFLISTFGCTSSDTEIKVNPPODFEIVDPGYLGYLQWQPLSLD 60  
 DB 1 MAFV--HIRCLFILTCTIGYS----LEIKVNPPODFEILDGILGYLQWKPPIVIE 54  
 QY 61 HFECEVEVELEKRNIGSETWKTITIKNLHKRGFDLKNKEIKHTLFPQCTNGSEVO 120  
 DB 55 KFGCGCLEVELEKRNVDSDWKITITRNLIKRGFDLKNKEIKHTLSEHGTNGSEVO 114  
 QY 121 SSAETTYTSPGIDETKQDMDCVYNNQYLLCSMKPGIGVLNMYLFTWYBESLDH 180  
 DB 115 SPTEISYIGSDSGSELETKQDMKCIYNNQYLLCSMKPKRTYSDNTYMFETBESLDH 174  
 QY 181 ALQCVDIYKADGONICRPFYLEASDYKDFYICVNGSSSENKPIRSSYFTPOLNIYKPLP 240  
 DB 175 ALQCAVYLDHDEKNVCKLSNLDSDYKDFEICVNGSSSKPIRSSYFTPOLNIYKPLP 234  
 QY 241 PVLITFTRESSCEIKLWSIPLGPIPARCFDYIEIREDDTLVLTATVEVETTLKTINE 300  
 DB 235 PEFLLHSIVENSIDIRKMKWSPGPIPPRCYTYEIVIREDDISWESATDKMDMLKRRANE 294  
 QY 301 TROLGVNSKVNIVYCSDDGIMSEWSDKQWCEDEDSKTKLLTFMPLPFGIILIVIVTG 360  
 DB 295 SEDLCEFFCKKVNIVYCADGIMSEWSEDEECGTYTGPDSKII-FIVPVCLFFILLLLLC 353  
 QY 361 LLLRKPNTPYKPM 372  
 DB 354 LIVEKEPEPTL 365

RESULT 12  
 W56252  
 ID W56252 standard; Protein: 157 AA.  
 AC W56252;  
 DT 16-SEP-1998 (first entry)  
 DE Interleukin-13 binding protein N-terminal ORF 1.  
 KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;  
 KM autoimmune disease; antibody; immunotherapy.  
 OS Homo sapiens.  
 FH Key  
 FT MISC\_difference 6 Location/Qualifiers  
 FT FT /note= "stop codon"  
 FT MISC\_difference 7 /label= "stop codon"  
 FT FT /label= "Unknown  
 FT MISC\_difference 17 /note= "Encoded by gtn"  
 FT FT /note= "stop codon"  
 FT Peptide 44..68  
 FT /note= "Putative signal sequence"  
 FT MISC\_difference 141 /label= "Unknown  
 FT FT

FT /note= "Encoded by cnt"  
 FT MISC\_difference 142 /note= "stop codon"  
 FT FT  
 W09910638-21  
 19-MAR-1998  
 10-SEP-1997; AV0591.  
 27-FEB-1997; AJ-005374.  
 19-SEP-1996; AJ-002262.  
 (AMRA-) AMRAD OPERATIONS PTY LTD.  
 P1 Hilton DJ, Nicola NA, Simpson RJ, Zhang J;  
 DR WPI: 98-207062/18.  
 DR N-PSDB: V22697.  
 PT New isolated interleukin-13 binding protein - used to develop  
 PT products for therapy e.g. for allergic conditions such as asthma or  
 PT for diagnosis or detection  
 PS Claim 7: Page 44; 65pp; English.  
 CC The IL-13 binding protein and related therapeutic molecules can be used  
 CC in the antagonism of at least one IL-13 activity. They can be used for  
 CC treating IL-13 mediated conditions such as certain allergic conditions  
 CC such as asthma or to inactivate locally administered IL-13 after IL-13  
 CC treatment. The products can also be used as diagnostic agents, e.g. for  
 CC detecting autoimmune diseases. The antibodies can also be used for  
 CC immunotherapy and may also be used as a diagnostic tool.  
 SQ Sequence 357 AA;

Query Match 21.7%; Score 456; DB 1; Length 157;  
 Best Local Similarity 77.2%; Pred. No. 2.4e-36;  
 Matches 86; Conservative 10; Mismatches 12; Indels 4; Gaps 3;

QY 1 MAFVCLAIGCLYFLISTFGCTSSDTEIKVNPPODFEIVDPGYLGYLQWQPLSLD 60  
 DB 43 MAFVCLAIGCLYFLISTFGCTSSDTEIKVNPPODFEIVDPGYLGYLQWQPLSLD 102  
 QY 61 HFECEVEVELEKRNIGSETWKTITIKNLHKRGFDLKNKEIKHTLFPQCTNGSEVO 120  
 DB 55 KFGCGCLEVELEKRNVDSDWKITITRNLIKRGFDLKNKEIKHTLSEHGTNGSEVO 114  
 QY 121 SSAETTYTSPGIDETKQDMDCVYNNQYLLCSMKPGIGVLNMYLFTWYBESLDH 180  
 DB 115 SPTEISYIGSDSGSELETKQDMKCIYNNQYLLCSMKPKRTYSDNTYMFETBESLDH 174  
 QY 181 ALQCVDIYKADGONICRPFYLEASDYKDFYICVNGSSSENKPIRSSYFTPOLNIYKPLP 240  
 DB 175 ALQCAVYLDHDEKNVCKLSNLDSDYKDFEICVNGSSSKPIRSSYFTPOLNIYKPLP 234  
 QY 241 PVLITFTRESSCEIKLWSIPLGPIPARCFDYIEIREDDTLVLTATVEVETTLKTINE 300  
 DB 235 PEFLLHSIVENSIDIRKMKWSPGPIPPRCYTYEIVIREDDISWESATDKMDMLKRRANE 294  
 QY 301 TROLGVNSKVNIVYCSDDGIMSEWSDKQWCEDEDSKTKLLTFMPLPFGIILIVIVTG 360  
 DB 295 SEDLCEFFCKKVNIVYCADGIMSEWSEDEECGTYTGPDSKII-FIVPVCLFFILLLLLC 353  
 QY 361 LLLRKPNTPYKPM 372  
 DB 354 LIVEKEPEPTL 365

## RESULT 13

R22216  
 ID R22216 standard; Protein: 396 AA.  
 AC R22216;  
 DT 22-JUL-1992 (first entry)  
 DE Sequence of human interleukin-5 receptor with signal peptide  
 DE (from a patient of eosinophilia).  
 KW Autoimmune disorder; therapy; eosinophilia.  
 OS Mouse.  
 FT MISC\_difference 47-475746-A;  
 FT 16-MAR-1992.  
 FT 11-SEP-1991; 308309.  
 FT 11-SEP-1990; DP-240638.  
 FT TAKATSU K.  
 FT Takatsui K, Tomimaga A, Takagi S, Murata Y;  
 FT WPI: 92-090329/12.  
 FT Human and murine interleukin-5 receptor and DNA encoding them  
 FT for treatment of auto-immune and eosinophilia conditions  
 FT involving IL-5  
 PS Claim 21: Page 42-44; 65pp; English.  
 CC The inventors claim: an isolated cDNA sequence encoding murine  
 CC (secretory) interleukin-5 (IL-5) receptor, which is synthesised from  
 CC murine early P cell mRNA; an isolated murine (secretory) IL-5  
 CC receptor; an isolated cDNA sequence encoding human (secretory) IL-5  
 CC receptor, which is synthesised from mRNA of human peripheral blood  
 CC eosinophil; and an isolated human (secretory) IL-5 receptor. Also  
 CC claimed are a COS monkey cell transfected with a recombinant vector  
 CC contg. the DNA; secretory human IL-5 lacking a cytoplasmic and a  
 CC transmembrane region; and an expression vector.  
 SQ Sequence 396 AA;

Query Match 14.8%; Score 311.5; DB 1; Length 396;  
 Best Local Similarity 26.6%; Pred. No. 6.2e-22;



QY 147 -----YNNQYLL-CSMRPGIGVLLDTNNLPY-----WYEGIDHALQCVYIKAD 191  
 Db 136 TMTEDNYSRLRSYQVSLHCTWLVGTFDAPEDTOYFLYRGSWTE-----ECQEYSKDT 189  
 QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSYTFQLONYVKPLPPYLLFTFR 248  
 Db 190 LGRNIACWFPRTFILSKGRDMLAVLVNGSSKSHAIRPFDOLFALHAIDQINPPLNTAEI 249  
 QY 249 ESSCEIRLKSIPUGPIPARCFDYEIEIRDDDTLVTAIVENETYLKTNETFQLOCFVY 308  
 Db 250 EGT-RLSIQMEKPVSAFPHCFDEYKIHNTRNQYLOIEKIMTNAFISIIDDLSKYDVQY 308  
 QY 309 RSKVNIYCSDDGIWSEWSDQCEGEDLSKRTLLRFVLPFGFILL-----VIFVTGL 362  
 Db 309 RAAVSSMCREAGLSEWS-QPIYGNDEHKP--LREW----FVIVIMATICFILLISLI 361  
 QY 363 LRKPNTYPMIP 374  
 Db 362 CKICHLWIKLFP 373

Search completed: January 19, 2000, 20:00:50  
 Job time: 8945 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 19, 2000, 13:58:11 ; Search time 71.05 seconds  
(without alignments)  
252.278 Million cell updates/sec

Title: US-09-077-817-2  
Perfect score: 2104  
Sequence: 1 MAFVCLAIQCLYFLISTF.....LLLRKPNTYPMIPEFCDT 380

Scoring table: BLOSUM62

Searched: 142080 seqs, 47169319 residues

Database: PIR\_62:\*

Word size: 0

Number of hits that pass the threshold: 142080

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID     | Description        |
|------------|-------|-------------|--------|----|--------|--------------------|
| 1          | 311.5 | 14.8        | 420    | 2  | S21052 | interleukin-5 rece |
| 2          | 311.5 | 14.8        | 396    | 2  | S21050 | interleukin-5 rece |
| 3          | 293   | 13.9        | 333    | 2  | S21053 | interleukin-5 rece |
| 4          | 292   | 13.5        | 335    | 2  | A40267 | interleukin-5 rece |
| 5          | 263   | 12.5        | 831    | 2  | J01655 | prolactin receptor |
| 6          | 247   | 11.7        | 415    | 2  | S12357 | interleukin-5 rece |
| 7          | 220   | 10.5        | 369    | 2  | A42565 | interleukin-2 rece |
| 8          | 216.5 | 10.3        | 830    | 2  | IS0455 | prolactin receptor |
| 9          | 212.5 | 10.1        | 369    | 2  | IA9280 | interleukin-2 rece |
| 10         | 208   | 9.9         | 373    | 2  | A57118 | interleukin-3 rece |
| 11         | 195   | 8.6         | 878    | 1  | A40091 | interleukin-3 rece |
| 12         | 180.5 | 8.6         | 897    | 1  | A39255 | cytokine receptor  |
| 13         | 178   | 8.5         | 896    | 1  | IS5653 | interleukin-3 rece |
| 14         | 173.5 | 8.2         | 896    | 1  | A35782 | cytokine receptor  |
| 15         | 165   | 7.8         | 581    | 2  | IA5971 | prolactin receptor |
| 16         | 165   | 7.8         | 610    | 2  | A34631 | prolactin receptor |
| 17         | 165   | 7.8         | 610    | 2  | A36116 | prolactin receptor |
| 18         | 165   | 7.8         | 412    | 2  | A41070 | prolactin receptor |
| 19         | 165   | 7.8         | 310    | 2  | A29884 | prolactin receptor |
| 20         | 160.5 | 7.6         | 303    | 2  | I77524 | prolactin receptor |
| 21         | 159   | 7.6         | 282    | 2  | I77525 | prolactin receptor |
| 22         | 159   | 7.6         | 608    | 2  | IS3269 | prolactin receptor |
| 23         | 151   | 7.2         | 206    | 2  | A57018 | prolactin receptor |
| 24         | 151   | 7.2         | 622    | 2  | A40144 | prolactin receptor |
| 25         | 150.5 | 7.2         | 917    | 2  | IA9699 | glycoprotein 130 - |
| 26         | 149   | 7.1         | 616    | 2  | A30304 | prolactin receptor |
| 27         | 142.5 | 6.8         | 400    | 2  | S06945 | granulocyte-macrop |
| 28         | 138   | 6.6         | 378    | 2  | A40266 | granulocyte-macrop |
| 29         | 134.5 | 6.4         | 1097   | 2  | SI7308 | leukemia inhibitor |
| 30         | 133.5 | 6.3         | 333    | 2  | SI3684 | granulocyte-macrop |
| 31         | 133.5 | 6.3         | 378    | 2  | S50040 | granulocyte-macrop |
| 32         | 131.5 | 6.2         | 630    | 2  | IS1086 | prolactin receptor |
| 33         | 129   | 6.1         | 150    | 2  | B34631 | lactogen receptor  |
| 34         | 126.5 | 6.0         | 918    | 2  | A36337 | membrane glycoprot |
| 35         | 122.5 | 5.8         | 286    | 2  | S50039 | granulocyte-macrop |

|    |       |     |       |   |        |                    |
|----|-------|-----|-------|---|--------|--------------------|
| 36 | 120.5 | 5.7 | 783   | 2 | JH0329 | granulocyte colony |
| 37 | 120.5 | 5.7 | 771   | 2 | B38252 | granulocyte colony |
| 38 | 120.5 | 5.7 | 863   | 2 | C38252 | granulocyte colony |
| 39 | 112.5 | 5.3 | 1630  | 2 | C41214 | protein-tyrosine-p |
| 40 | 111.5 | 5.3 | 1557  | 2 | D41214 | protein-tyrosine-p |
| 41 | 110   | 5.2 | 6805  | 2 | S20901 | titin - rabbit (fr |
| 42 | 109.5 | 5.2 | 26926 | 1 | I38344 | titin, cardiac mus |
| 43 | 109.5 | 5.2 | 918   | 2 | A44257 | interleukin-6 sign |
| 44 | 107.5 | 5.1 | 638   | 2 | A33991 | somatotropin recep |
| 45 | 107.5 | 5.1 | 638   | 2 | S04530 | somatotropin recep |

#### ALIGNMENTS

RESULT 1

S21052

Interleukin-5 receptor alpha chain precursor (clone lambda hSR.12), membrane-anchored

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Feb-1998

C:Accession: S21052; A46175

R:Morata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tomimaga, A.; Takatsu, K.

T:Exp. Med. 175, 341-351, 1992

A:Title: Molecular cloning and expression of the human interleukin 5 receptor.

A:Reference number: S21050; MUID:92121815

A:Accession: S21052

A:Molecule type: DNA

A:Accession: 1-420 <MOR>

A:Cross-references: EMBL:X61176; NID:933943; PID:933844

A:Experimental source: Clone lambda hSR.12

R:Verheer, J.; Tuypens, T.; Plaetnick, G.; Verhee, A.; Fiers, W.; Devos, R.

Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992

A:Title: Molecular basis of the membrane-anchored and two soluble isoforms of the hum

A:Reference number: A46175; MUID:92357767

A:Accession: A46175

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 333-420 <TAV>

A:Experimental source: HL-60 cells and eosinophils

A:Note: sequence extracted from NCBI database (NCBI:116243, NCBI:116244)

C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-430/Domain: interleukin-5 receptor alpha chain #status predicted <MAY>

F:435-365/Domain: transmembrane #status predicted <TM>

F:333-131,137,142,216,244/Binding site: carbohydrate (asn) (covalent) #status predicte

Query Match 14.88; Score 311.5; DB 2; length 420;

Fast Local Similarity 26.98; Pred. No. 2.3e-17;

Matches 100; Conservative 69; Mismatches 156; Indels 47; Gaps 16;

27 DFEKVNPPQPEFVDPGLYLQWOPPLSLDFKCYEYELKYNISSEMTKITIT 86

25 DEKISLPPVNFITKVTG-LAQVLLQWKPNDQO-RNVNLEYQKINAPREDEYERIT 82

87 KNLVKKDFGDKGFEAKIHTLLPMOCNGSEVOSSNATETTYWSPOGIFETKVDMDCV 146

83 ES--KCYTILHKGFSASVRIILO---NDHSLASSWASAEIHL-APPSPGTSVYNLCIT 135

147 -----YNNQCYLL-CSMKPGIGVLLDTNNTLFY---WTEGDLHALQCVYIKAD 191

136 TITTFPDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRGSWME-----ECQYSKDT 189

192 -CGNIGCTP--YLEASDKFYICVNGSSNNKPRSSYFFQOLNLYKPLPYVLTFR 248

190 LGRINACWFPPTFLISKGRDLAVLVNNGSKSAIRPDQALAHAIQINPPLVTAEI 249

749 ESSEIKFKWGISPLGPIARCQFEIREDDTLVATVENETTLTKTNETROLGVV 308

250 EGT-KLSIQWKEKPVSAPIHCFDEVKIHNTRNGYLQLEKMTNAFIISIDLSKYDVQV 308

309 RSKVNIYCSDDGIWSEMSDKQCPGEGDLSKRTLLRFWLPFGFIIL-----VIFVTCIL 362

DB 309 RAAVSMCREAGIMSEMS-QPIYVGNDEHNP--LREM---FVIYIMATICFILLILSLI 361  
 QY 363 LKRPNTYPMIP 374  
 DB 362 CRICHLMIKILFP 373

## RESULT 2

S21050  
 Interleukin-5 receptor alpha chain precursor (clone lambda h5R.27) - human  
 C.Species: Homo sapiens (man)  
 C.Date: 29-Jan-1998 #sequence-revision 06-Feb-1998 #text-change 05-Jun-1998  
 C.Accession: S21050; S78106  
 R.Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tomimaga, A.; Takatsu, K.  
 J. Exp. Med. 175, 341-351, 1992  
 A.Title: Molecular cloning and expression of the human interleukin 5 receptor.  
 A.Reference number: S21050; MUID:92121815  
 A.Accession: S21050  
 A.Molecule type: DNA  
 A.Residues: 1-396 <MUR>  
 A.Cross-references: EMBL:X61177; NID:933839; PID:933840  
 A.Experimental source: clone lambda h5R.27  
 R.Murata, Y.  
 submitted to the EMBL Data Library, July 1991

A.Reference number: S78106  
 A.Accession: S78106  
 A.Molecule type: DNA  
 A.Residues: 1-128, 'I', 130-396 <MUR>  
 A.Cross-references: EMBL:X61177; NID:933839; PID:933840  
 C.Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein  
 F:1-20/Domain: signal sequence #status predicted <Sig>  
 F:21-396/Product: interleukin-5 receptor alpha chain #status predicted <MAT>  
 F:345-365/Domain: transmembrane #status predicted <TM>  
 F:35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.8%; Score 311.5; DB 2; Length 396;

Best Local Similarity 26.9%; Pred. No. 2, 2e-17;  
 Matches 100; Conservative 69; Mismatches 156; Indels 47; Gaps 16;

QY 27 DPEIKNPDPDEIVPGYGLYILOWOPPLSDHKECEVELEKYNIGSTWTTIT 86  
 DB 25 DEKISLPVNFIFIKYTG-LAOVLLQMKRPDQO-RNVNLEQVKNAPKEDYETRT 82  
 QY 87 KNLHYDGFDLNKGIAKHTLLPMQCTNGSEVOSSMAETTYWISPGIPEYKQDMDCV 146  
 DB 83 ES---KCVIILKHGFSASRTILQ---NDHSLASSMAAEHL-APPGSGISVNVLTCT 135  
 QY 147 -----YNNQYLL-CSWKPFGIGVLLDTNYNLFY---WYEGLDHALOCVDYIKAD 191  
 DB 136 TWTEDNYSRLNSYQVSLCHTWMVGTDAPEDQYFLYRGSWTE-----ECQERSKDT 189  
 QY 192 -GONIGCRPP--YLEASDKDPIYICVNGSSENPPISSYTFPOLQNTVPLPVYILFTR 248  
 DB 190 LGRNIAQWPFRTFILLKSGDWLAVLVNGSSKHSARPFQDLFALHIDQINPLANTAEI 249  
 QY 249 ESSCEIKLMSIPDIPARCFEYIEIRDDTTLVATVENETYLKTNERTROLCPVY 308  
 DB 250 EGT-RLSIQMERKVSAPFPHCFEYEVKINTRNGYIQIEKMTNATISIIDLSKIDVQY 308  
 QY 309 RSKVNITCSDDGIMSEMSKQCEGSDLSKTLIRFWLPFGFILL-----VIFVTGL 362  
 DB 309 RAAVSMCREAGIMSEMS-QPIYVGNDEHNP--LREM---FVIYIMATICFILLILSLI 361  
 QY 363 LKRPNTYPMIP 374  
 DB 362 CRICHLMIKILFP 373

## RESULT 3

S21053  
 Interleukin-5 receptor precursor soluble (clone lambda h5R.25) - human  
 C.Species: Homo sapiens (man)

C.Date: 29-Jan-1998 #sequence-revision 06-Feb-1998 #text-change 20-Feb-1998  
 C.Accession: S21053; S78107  
 R.Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tomimaga, A.; Takatsu, K.  
 J. Exp. Med. 175, 341-351, 1992  
 A.Title: Molecular cloning and expression of the human interleukin 5 receptor.  
 A.Reference number: S21053; MUID:92121815  
 A.Accession: S21053  
 A.Molecule type: mRNA  
 A.Residues: 1-333 <MUR>  
 A.Cross-references: EMBL:X62156; NID:936465; PID:936466  
 A.Experimental source: clone lambda h5R.25  
 R.Murata, Y.  
 submitted to the EMBL Data Library, September 1991

A.Reference number: S78107  
 A.Accession: S78107  
 A.Molecule type: mRNA  
 A.Residues: 1-128, 'I', 130-333 <MUR>  
 A.Cross-references: EMBL:X62156; NID:936465; PID:936466  
 C.Keywords: alternative splicing; cytokine receptor; glycoprotein  
 F:1-20/Domain: signal sequence #status predicted <Sig>  
 F:21-333/Product: interleukin-5 receptor #status predicted <MAT>  
 F:35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.9%; Score 293; DB 2; Length 333;

Best Local Similarity 28.3%; Pred. No. 5, 1e-16;  
 Matches 90; Conservative 55; Mismatches 139; Indels 34; Gaps 12;

QY 27 DPEIKNPDPDEIVPGYGLYILOWOPPLSDHKECEVELEKYNIGSTWTTIT 86  
 DB 25 DEKISLPVNFIFIKYTG-LAOVLLQMKRPDQO-RNVNLEQVKNAPKEDYETRT 82  
 QY 87 KNLHYDGFDLNKGIAKHTLLPMQCTNGSEVOSSMAETTYWISPGIPEYKQDMDCV 146  
 DB 83 ES---KCVIILKHGFSASRTILQ---NDHSLASSMAAEHL-APPGSGISVNVLTCT 135  
 QY 147 -----YNNQYLL-CSWKPFGIGVLLDTNYNLFY---WYEGLDHALOCVDYIKAD 191  
 DB 136 TWTEDNYSRLNSYQVSLCHTWMVGTDAPEDQYFLYRGSWTE-----ECQERSKDT 189  
 QY 192 -GONIGCRPP--YLEASDKDPIYICVNGSSENPPISSYTFPOLQNTVPLPVYILFTR 248  
 DB 190 LGRNIAQWPFRTFILLKSGDWLAVLVNGSSKHSARPFQDLFALHIDQINPLANTAEI 249  
 QY 249 ESSCEIKLMSIPDIPARCFEYIEIRDDTTLVATVENETYLKTNERTROLCPVY 308  
 DB 250 EGT-RLSIQMERKVSAPFPHCFEYEVKINTRNGYIQIEKMTNATISIIDLSKIDVQY 308  
 QY 309 RSKVNITCSDDGIMSEMS 326  
 DB 309 RAAVSMCREAGIMSEMS 326

## RESULT 4

A40267  
 Interleukin-5 receptor alpha chain precursor - human  
 C.Species: Homo sapiens (man)  
 C.Date: 17-Jan-1992 #sequence-revision 17-Jan-1992 #text-change 10-Sep-1997  
 C.Accession: A40267  
 R.Savarnier, J.; Devos, R.; Cornelis, S.; Tuyenens, T.; Van der Heyden, J.; Piers, W.;  
 Ceil 66, 1175-1184, 1991  
 A.Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-sp  
 A.Reference number: A40267; MUID:92005669  
 A.Accession: A40267  
 A.Status: preliminary  
 A.Molecule type: mRNA  
 A.Residues: 1-335 <TAV>  
 A.Cross-references: GB:M75914; NID:9186387; PID:9186388  
 C.Keywords: cytokine receptor; transmembrane protein

Query Match 13.9%; Score 292; DB 2; Length 335;  
 Best Local Similarity 28.0%; Pred. No. 6, 2e-16;

Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;

QY 27 DTEIKVNPDDFIYDPGYLYLQWQPLSLDHFKECEVEYELKRNIGSEWTKIIT 86  
 DB 25 DEKISLPPVNFYIKVTG-LAQVLLQWKPNDPOQ-RNVNLEOVKNAPREDYERIT 82  
 QY 87 KNLHYDGFDLNGIGIAKIHITLLPWQCTNGSEVOSSWAETTYWISPOGIBETKODMDCV 146  
 DB 83 ES---KCVTLHKGFSASVTLIQ---NDHSLASSMAKSELH-APGSPGTSIVNLCT 135  
 QY 147 -----YVMQYLL-CSMKPGIGVLLDTNINLFY-----WEGIDHALQCVDIKAD 191  
 DB 136 TATTEEDNYSRLRSYOVSLHCTMTLVGTDPADPDQYFLFYRYSWTE-----ECOEYSKDT 189  
 QY 192 -GONIGCRFP--VLEASDYADFYICVNGSENNKPIRSSYTFPOLQNTVKKLPYVLTFR 248  
 DB 190 LGNNIACWEPRTILSLGRDWLSVLVNGSSKSHAIRFDOLFALHAIQDQINPLNVAEI 249  
 QY 249 ESSCEIKLAKSIPLGPICPARCFDEIREDDTLVATVATVENEYTLTKTNETRQLCFV 308  
 DB 250 EGT-RLSIQMEKRVSAFPIHCIPDEYKIHNTKNGYLOIEKLMNAFISIIDLSKYVOY 308  
 QY 309 RSKVNYICSDDGIMSEWS 326  
 DB 309 RAAVSSMCREAGIMSEWS 326

## RESULT 5

QJ01655  
 prolactin receptor precursor - chicken  
 C/Species: Gallus gallus (chicken)  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 10-Sep-1997  
 C/Accession: J01655  
 R.Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.  
 Biochem. Biophys. Res. Commun. 188, 490-496, 1992  
 A/Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA se  
 A/Reference number: J01655; M0ID:93075121  
 A/Accession: J01655  
 A:Molecule type: mRNA  
 A:Residues: 1-831 <TRAN>  
 A:Cross-references: DDBJ:D13154; NID:g222848; PID:d1002939; PID:g222849  
 A:Experimental source: Kidney  
 C/Keywords: glycoprotein; transmembrane protein  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-831/Product: prolactin receptor #status predicted <DAT>  
 F:439-460/Domain: transmembrane #status predicted <TM>  
 F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (covala

Query Match 12.5%; Score 263; DB 2; Length 831;

Best Local Similarity 26.4%; Pred. No. 3 8e-13;

Matches 103; Conservative 58; Mismatches 183; Indels 46; Gaps 17;

QY 18 TTFGCTSSDTEIKVN--PPDPE---YVDPG-----YLGVLQWQPLSL 59  
 DB 97 TTFNITVATNEIGNSSDPQYDVATSIQPGSPVNLTEFKRSANIMYIAKMSPELLA 136  
 QY 60 DHKECTVELEKRYNIGSTTKTITIKNLAKYDGFPLNGIEAKITLLPWQCTNGSEV 119  
 DB 157 DASSNHLNHYELIKRKEKEWETI---SVGVQTOCKIN-LNAGMYVVOVVKRDTLDPGE 212  
 QY 120 QSSMAETTYWISPOG-IPEKKVODMDCVYVNMQYLLCSMKPGIGVLLDTNINLFYWEGL 178  
 DB 213 WSMMSSEKRLILISGSGSPKPKITIKRSPKEKTFQWMPGLDGGPTVITLLISKEGE 272  
 QY 179 DHALQCVDIKADQONIGCFPLEASDYKDFYICVNGSENNKPIRSSYTFPOLQNTVKK 238  
 DB 273 EGYVECPDY-RTAGPN-SCFYDKKHTSEFTIYNITVATNEMGSSSDPHYDVYTIYOP 330  
 QY 239 LPVYILTFRESCEIK----LKMS-IPGPICPARCFDEIETR---EDDTLVATVAVEN 290  
 DB 331 DPEVNTLLEIKRKPIKRYLVLTWSEPLADVBSGWLTLLEYELRLKREGEWETITVQ 390

QY 25 ET-VLEKTNETROLCEVSVSKVNYICSD--GIWSEMSDKOCW-GEDESKTLLREWL 346  
 DB 391 QIQYKMSLNPKKYYI-----IQIHCKPDHGSMSMSSENNTQIINDRYADM-VWI 443  
 QY 367 PEGFT-LILVIFVTGILKKRPNTYKMP 374  
 DB 444 VLGVASSLIQILMSMTVWLKGYRITFMLP 473

## RESULT 6

EJ12357  
 Interleukin-5 receptor - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Mar-1998  
 C/Accession: S12357  
 R.Takaki, S.; Tomioka, A.; Hiroshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu  
 EMBO J. 9, 4367-4374, 1990  
 A/Title: Molecular cloning and expression of the murine interleukin-5 receptor.  
 A/Reference number: S12357; M0ID:91092260  
 A/Accession: S12357  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-415 <TAK>  
 A:Cross-references: GB:D90205; NID:g220465; PID:d1014936; PID:g220466  
 C/Keywords: cytokine receptor; transmembrane protein

Query Match 11.7%; Score 247; DB 2; Length 415;

Best Local Similarity 24.6%; Pred. No. 3e-12;

Matches 91; Conservative 70; Mismatches 151; Indels 58; Gaps 18;

QY 34 PDDEFIVDQGYLYLQWQPLSLDHFKECEVEYELKRNIGSEWTKIITKRLHYKD 93  
 DB 29 PPNVFTIKATG-LAQVLLHMDPNPDOQ-RVDELYVKNAPQEDYTRKIES---KC 83  
 QY 94 GFLNKGIEAKIHITLLPWQCTNGSEVOSSWAETTYWISPOGIBETKODMDCVYVN--- 150  
 DB 84 VTLPEGEFASVRLIK---SSHITLASSWVSAEL-KAPGSPGTSVNTLCTHTVSS 139  
 QY 150 -----WQY-LICSMKPGIGVLLDTNINLFYWEGLDHALQCVDIK-ADGONIGCFP- 201  
 DB 140 HTHLRPYQVSLRQTLWVGKNDAPEDTOYFLYIRGVILE--KCOEYSDALNRYTACWEP 197  
 QY 201 -VLEASDYKDFYICVNGSENNKPIRSSYTFPOLQNTVKKLPYVLTFRSSCEIKLMS 259  
 DB 198 TRINSGFEDLAHINSSSRAAIKPPDQLSPALDQVNPNNVYELISN-SLYIQWE 256  
 QY 260 TPLGPICPARCFDEIREDT-----TTLVATVATVENEYTLTKTNETRQLCFV 308  
 DB 257 KPLSAPFDHCFENNELKIYNNKKNHICKELIANKFISKIDVSTISQ-----V 305  
 QY 305 RSKVNYICSDDGIMSEMSDKOCWEGEDLSKTLIREW---LDFPILLIVITVGLLR 364  
 DB 306 RAAVSSPCRRMGRGMEWS-OPITYGRE--RKSLVE-WHLIVLPACAFVLLF--SLICR 359  
 QY 365 KPNYTPKMP 374  
 DB 360 VCHLWTRLP 365

## RESULT 7

A42565  
 Interleukin-2 receptor gamma chain - human  
 C/Species: Homo sapiens (man)  
 C/Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
 C/Accession: A42565; A46591; I54332  
 R.Takahata, T.; Asao, H.; Ohnami, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Murakata, H  
 Science 257, 379-383, 1992  
 A/Title: Cloning of the gamma chain of the human IL-2 receptor.  
 A/Reference number: A42565; M0ID:92335883  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid; protein

A:Residues: 1-369 <TAK>  
 A:Cross-references: GB:D11086; NID:g303611; PIDN:BA01857.1; PID:dl002334; PID:g219890  
 A:Experimental source: MOLT beta lymphoid cells  
 A:Note: sequence extracted from NCBI backbone (NCIP:109167)  
 R:Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.  
 J. Biol. Chem. 268, 13601-13608, 1993  
 A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.  
 A:Reference number: A46591; MUID:93293887  
 A:Accession: A46591  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-369 <RES>  
 A:Cross-references: GB:U12183; NID:g307056; PIDN:AAA59145.1; PID:g307058  
 R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.; He  
 Hum. Mol. Genet. 2, 1099-1104, 1993  
 A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-linked  
 A:Reference number: I54332; MUID:94004847  
 A:Accession: I54332  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-369 <RE2>  
 A:Cross-references: GB:U19546; NID:g349631; PIDN:AA37524.1; PID:g349632  
 C:Genetics:  
 A:Gene: GDB:112RG; SCIDX1: IMD4  
 A:Cross-references: GDB:134807; OMIM:308380  
 A:Map position: Xq13.1-Xq13.1  
 A:Intons: 39/1, 90/2, 152/1, 198/3, 253/1, 285/2, 308/3  
 A:Note: defects are associated with an X-linked form of severe combined immunodeficiency  
 C:Superfamily: interleukin-2 receptor gamma chain  
 C:Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunodeficiency

Query Match 10.5%; Score 220; DB 2; Length 369;  
 Best Local Similarity 25.5%; Pred. No. 3,5e-10;  
 Matches 70; Conservative 48; Mismatches 121; Indels 36; Gaps 11;

QY 97 LNKGIKAKHITLIPMCCTNISE-VQSSMAETTYWISPGIPEKRVQDMCVYNNQYLIC 155  
 DB 19 LGVGLMTTLT-----PQNEPTTADFTLTPTDLSVSTLPLEVOCFVNVEMMC 72  
 QY 156 SW-----KPGIGVLLDTVYNLEFYWEGLDH--ALQCVIRKADGONIGCRPFYLEASDY 207  
 DB 73 TNNSSSEPP-----TNLTHTWTKNSNDKAVQCSHLESEETISGQLOKKEHLH 125  
 QY 208 KDFYICVNGSSSEKPIRSSYFTFQLOINIVKPLPVYLTFTRESSCEIKLWSIPLGPIPA 267  
 DB 126 QTFVVOLODPRE--PRQATQMLKQNLVTPMAPENLTLHKLSESOLELWN--NRFLN 180  
 QY 268 RCFDYIEIRED-DTLLVATVE-NETYLKTINETROLCFVVRKAVNIYCSDDGIWSEW 325  
 DB 181 HCLEHLVQRTDMDHSWTEDOSVDYRHRKFLSPVDGQRRTYFRVRSRNPICGSAQHWSEW 240  
 QY 326 SDQKWEGEDLSKRTLLRFMLPGFILLIIVFYTG 360  
 DB 241 SHPIHW-GSNTSKEN-----PLFLALEAVVISVG 268

RESULT 8  
 150455  
 prolactin receptor - pigeon  
 C:Species: Columba livia (domestic pigeon)  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 13-Sep-1996  
 C:Accession: I50455  
 R:Chen, X.; Horseman, N.D.  
 Endocrinology 135, 269-276, 1994  
 A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.  
 A:Reference number: I50455; MUID:94483267  
 A:Accession: I50455  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-830 <CHE>  
 A:Cross-references: EMBL:U07694; NID:g466381; PID:g466382

Query Match 10.3%; Score 216.5; DB 2; Length 830;  
 Best Local Similarity 24.4%; Pred. No. 1.9e-09;  
 Matches 93; Conservative 53; Mismatches 174; Indels 61; Gaps 16;

QY 18 TTRGCTSSDTEIKVPPQDFEIVDGYLG-----YIYLDN 53  
 DB 97 TTYNTIVMANNELGNSNS-----DQYVDVTSIVQDPAVNLSTETKTSASTYTLIAKW 150  
 QY 54 QPPLSLDHEFECEV-ETELKYRNIGSEFTWITTKMLHAKDGFGLNKIGIEAKITTLPMQ 112  
 DB 151 SPPPLADVTSNSHYVYKELRLKPEKEEMETV---SVGQTOYQYKVR-LQAGKYVVOVR 206  
 QY 113 CTNGSEVQSSMAETTYWISPG-IPEKRVQDMCVYNNQYLCSWKPGLVLDNTNML 171  
 DB 207 CVLDIGEMSWSESRHIIHPNGESPPEKPTLIICRSEKETFCWKRPGSDGHPNTYTL 266  
 QY 172 FYTEGLDHALQCVDIKADGONIGCRPFYLEASDYKDYICVNGSSSEKPIRSSIFTQ 231  
 DB 267 LYSKEGEERYECEDY-KTAGPN-SCYFDRKHTSEFTIYINITYKATNEIGSNVSDPLYVD 324  
 QY 232 LQNVKPLPVYLTFTRESSCEIK---LKWS-IPGPIPA--RCFDYETIREDDTLY 284  
 DB 325 VYIYOTDPPVANTLELKTIVNRKPIVLTLWSPPLADRSGLTIDYELRLKPEA--- 382  
 QY 285 TATVENEYTLKTTNETROLCFVY---RSKVNIGSD--GIWSEMS-DKQCEGEDLS 337  
 DB 382 -----PEWETIFVQGOQTHKMSLNGKKYIVQIHCKPDHGSMSWSLEKYLQIPTDR 436  
 QY 338 KTLIRFMLPGFILLIIVFY 358  
 DB 437 IKDMV-VWIIIVGLSSLICLV 456

RESULT 9  
 149280  
 interleukin-2 receptor gamma chain precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 27-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 23-Jul-1999  
 C:Accession: I49280; A47514; JN0775; S37582; I53398  
 R:Cao, X.; Kozak, C.A.; Liu, Y.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993  
 A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R)  
 A:Reference number: A47514; MUID:93391374  
 A:Accession: I49280  
 A:Molecule type: DNA  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Residues: 1-369 <CAO>  
 A:Cross-references: EMBL:U21795; NID:g727349; PIDN:AAA64279.1; PID:g727350  
 A:Accession: A47514  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-369 <RE2>  
 A:Cross-references: GB:U20048; NID:g404067; PIDN:AAA39286.1; PID:g404068  
 R:Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.  
 Biochem. Biophys. Res. Commun. 193, 356-363, 1993  
 A:Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of fu  
 A:Reference number: JN0592; MUID:93277575  
 A:Accession: JN0592  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-369 <KUN>  
 A:Cross-references: DBJ:D13565; NID:g303684; PIDN:BA02760.1; PID:dl003265; PID:g303  
 R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.  
 Gene 130, 303-304, 1993  
 A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.  
 A:Reference number: JN0775; MUID:93366191  
 A:Accession: JN0775  
 A:Molecule type: mRNA  
 A:Residues: 1-369 <KOB>  
 A:Cross-references: GB:D13821; NID:g436045; PIDN:BA02974.1; PID:dl003480; PID:g43604  
 R:Chiu, R.K.; Dougherty, G.J.  
 submitted to the EMBL Data Library, October 1993





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OY 139 KVQDMDCVYNNQWYLLCSMKPGIGVLLDTNNALFYWEGDLHALQCVDYIKADGONI---196
D 248 QPQNLQCFDFDQISLHCEMEWOTOTGTSVSFLFRPSPAAREKCSFVKKRQASVYTR 307
OY 196 -GCRPPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQLONIYKPLPPYV-LTFRESSCE 253
D 308 YRCSLPVPEPSAHSQYTSVKHLQEGKFI-MSYHIOME-----PRLINQTKNRDS---358
OY 254 IKLWISILGPAPARCFD--VEIEIRDDTLVTATVEN-----ETTLTKTNETQOLCFV 307
D 358 YSLHETQKIP---KYIDHTFOYTKKSESCKSKSTKTELGAVNSMDLPQLEPDTSYCAR 414
OY 308 VRSK-VNIYCSDDGIMSEMSDKOCWEGEDLSKRTLLRFWLPFGFILLIYIVTGLL 363
D 415 VVRKISDY---DGIWSEMSNEYWT-TDWVWPTL---WI-----VLLIVFLITL 460

RESULT 12
A39255
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997
C:Accession: A39255
R:Hayashida, K.; Kitamura, T.; Gorman, D.M.; Aral, K.; Yokota, T.; Miyajima, A.
Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
A:Title: Molecular cloning of a second subunit of the receptor for human granulocyte-mac
A:Reference number: A39255; MUID:91086871
A:Accession: A39255
A:Molecule type: mRNA
A:Residues: 1-897 <HAT>
A:Cross-references: GB:M38275
C:Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-specific
C:Genetics:
A:Gene: GDB:CSF2RB
A:Cross-references: GDB:126638; OMIM:138981
A:Map position: 22q13.1-22q13.1
C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: alternative splicing; cytokine receptor; duplication; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-897/Product: cytokine receptor common beta chain #status predicted <EXT>
F:17-444/Domain: extracellular #status predicted <EXT>
F:325-233/Domain: cytokine receptor homology <CRS1>
F:250-431/Domain: cytokine receptor homology <CRS2>
F:444-460/Domain: transmembrane #status predicted <TM>
F:461-897/Domain: intracellular #status predicted <INT>

Query Match 8.6%; Score 180.5; DB 1; Length 897;
Best Local Similarity 22.6%; Pred. NO. 1.5e-06;
Matches 90; Conservative 58; Mismatches 146; Indels 105; Gaps 21;

OY 32 VNPDPDFEIVDGYLGY-----LYLOMOP-----LSDDH-----63
D 97 VIPQCSFVTVTDVYSFQDPRDLGRLVYTLQHVQPPRPLQISTDDHLLWMSVAL 156
OY 63 -----KECTVEYELKRYNIGSETW--TIITKNLHKDGFDLNKGE-----A 103
D 157 GSPQSHMLSPGDLFEFEVYKRL-QDSMEDAAILLSTNS-----QATLGEHMLPSTYVA 210
OY 104 KIHT-LLMQCINSGSEVSSAETTYWISPOGIPETKQVDMDCVYNNQWYLLCSMKPGIG 162
D 211 RVRTRLAGSRLSGR--PSKMSPEVCWDSQPG-DEAQPQNLCECFDGAAYVLSGSWEVRKE 267
OY 163 VLDNTNNLFYWEGDLHALQCVDYIKADGONI-----CRPYLEASDYKDFYICVN 215
D 268 VASSVSFGFLFPSPDAGEECSPVLR---EGLGLHTRHHCQIPVPDPATGQIVSYVO 324
OY 216 GSSENKPIRSSYFTFQLONIYKPLPPYVLTFTRESSCEIKLWMSIPLGPIPARCDYEIE 275
D 325 PRRAKHKIKSSV-----NI--QMAPPSLNTYKDDG-SYSLWEMMKMYEHIDHFEIQ 375
OY 276 IREDDTLVTAT-VENEYITLKTNN-----ETROLCFV-VSKVNIYCSDDGIMSE 324

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D 376 YRKD-----TATWKSKEITLQNAHSMALPALPESTRTMARVVRTSRTGY---NGIMSE 427
OY 325 WSDKOCWEGEDLSKRTLLRFWLPFGFILLIYIVTGLL 363
D 428 WSEARSDTESV-----LPMWVTLIVIFLITAVL 457

RESULT 13
A35653
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C:Accession: I56563
R:Appel, K.; Buttin, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A:Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia
A:Reference number: I56563; MUID:95370942
A:Accession: I56563
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-896 <RES>
A:Cross-references: GB:S79263; NID:q1086954; PIDN:AA35068.1; PID:q1086955
C:Genetics:
A:Gene: rIL-3Rbeta
C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: cytokine receptor
F:39-235/Domain: cytokine receptor homology <CRS1>
F:253-433/Domain: cytokine receptor homology <CRS2>

Query Match 8.5%; Score 178; DB 2; Length 896;
Best Local Similarity 21.4%; Pred. No. 2.3e-06;
Matches 87; Conservative 65; Mismatches 167; Indels 88; Gaps 21;

OY 5 CLAIGCL-YR-FLISTTFGCTSSSDTEIKYN-----PRDFEIVDGYLGYL 49
D 94 CVPRRCVLPYQFVSFKEDYSLQDRLSLHLVLAQHVQPPPKDISISPG--DHF 151
OY 50 YLOMOPPL-----SLDFKCEYVEYELKRYNIGSETWKTITTNLHKDGFDLNKGEIAKH 106
D 152 LKWSVPLGDAVSLISKQIOFEVAYKQL-QDSLH-----TCNLWVTLPEK 203
OY 107 TLPL-----WQCTNGSEVQ---SSMAETTYWISPOGIPETKQVDMDCVYNNQWYLL 154
D 204 LFLPSIVARVAKQALABGSSLSGRPSGMSPEVHWDSPTE-DKARPQYLQCFFGIQLN 262
OY 155 CSMKPGIGVLDNTNNLFYWEGDLHALQCVDYIKADGONICRPPYLEASDYKDFYICV 214
D 263 CSWEYWFRTVTSVSGLFYSPPRAGEKCSPVKE-----LQASRYTRHCSL 311
OY 215 NGSSSENKPIRSSYFTFQLONIYKPLPPYVLTFTRESSCEIKLWMSIPL 262
D 312 NVSD---FAHSQYIVSVKRLQEGKFIESFNHICQNPPTLILNKRDS---YSLHWEQK 365
OY 263 GPIPARCFDYEIEIR-----EDDTLVATAVENETTYLKTNETROLCFVVRKSVNIYC 316
D 366 MSYPIQHAQFQYQYKKLDRWEDSKT-----ENLNHAHSMDLPOLEPGTSCARVAVKTI 421
OY 317 SDDGIMSEMSDKOCWEGEDLSKRTLLRFWLPFGFILLIYIVTGLL 363
D 422 EYKGLSEMSENECTWT-TDWVWPTL---WI-----VLLIVFLITL 460

RESULT 14
A35782
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A35782
R:Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Aral,
Proc. Natl. Acad. Sci. U.S.A. 87, 5453-5463, 1990
A:Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like pro

```

A:Reference number: A35782; MCID:90319131  
 A:Accession: A35782  
 A:Molecule type: mRNA  
 A:Residues: 1-896 <GOR>  
 A:Cross-references: GB:M34397; NID:q191821; PIDN:AAA37204.1; PID:q309101  
 C:Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 receptor  
 C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology  
 C:Keywords: cytokine receptor; duplication; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <Sig>  
 F:23-96/Product: cytokine receptor common beta chain #status predicted <Mat>  
 F:23-44/Domain: extracellular #status predicted <Ext>  
 F:39-235/Domain: cytokine receptor homology <CRS1>  
 F:253-434/Domain: cytokine receptor homology <CRS2>  
 F:442-463/Domain: transmembrane #status predicted <TM>  
 F:464-896/Domain: intracellular #status predicted <Int>

Query Match 8.2%; Score 173.5; DB 1; Length 896;  
 Best Local Similarity 20.7%; Pred. No. 5.2e-06;  
 Matches 81; Conservative 69; Mismatches 185; Indels 57; Gaps 18;

QY 5 CLAIGLTYFLITSTFGCTSSDTEIKVNPQDEIYDPIGLY 48  
 DB 94 CVPRRCVIPPTRSTINEDIYSFRPDSDLGIQLMVPILAQNVPPLPRNVSISSEDR 150  
 QY 49 LYIQMOPLSLDHFKETVEYELKYNIGSEFWKTIITKNLHYKDFDLNKG 100  
 DB 151 FLEHMSVSLGDAQVSWLSKDIEFVAAYKRLQDSMEDASLHSTSKQVFEKFLPNS 209  
 QY 101 IEA-KIHT-LLPQCTNGSEVOSSMAETTYWISPGIPEKVDMDCVYNNMOYLCSWK 158  
 DB 210 IYAPRYRTRLYPGSSLSGRPSRWSPPEAHMDQPGDKAQPNLQCFEFGIQLHCSWE 266  
 QY 159 PGIGVLDITNINNFYWEGLDHALOCVDYIKADGONI--GCRPYLEASDYKDFYIC 213  
 DB 267 VMTQTGSVSFGFLYPPSPAPAEKCSVPVKEPPGASVTRYHCSLVPPEASHQSQTYS 326  
 QY 214 VNGSENKPIRSSYFTFOLNIYKPLPPVYLFTFTRESSCEIKLWSIFLGPAPRCFDE 273  
 DB 327 V-----KHLQCKFLMSYNIQMEPTLNLTKNRDS--YSLHMETQKMAYSFIEHTFQ 377  
 QY 274 IETREDDTLVATVEN--ETYLKTTNETRQLCFYVRKVNINICSDDGIMSEMSDKQW 331  
 DB 378 VOYKKKSDSEWDSKTEMLDRAHSMDSOLEPDTSCARAVKPIISNYDGIMSKSEETW 437  
 QY 332 EGEDLSKTLIRFMLPGFILLIYVFTGILL 363  
 DB 438 K-TDWVWPTL--WT---VLIVFLILTL 461

RESULT 15  
 145971  
 prolactin receptor - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 28-Feb-1997  
 C:Accession: 145971  
 R:Scott, P.; Kessler, M.A.; Schuler, L.A.  
 Mol. Cell. Endocrinol. 89, 47-58, 1992  
 A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin  
 A:Reference number: 145971; MCID:93446019  
 A:Accession: 145971  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-581 <SCO>  
 A:Cross-references: GB:L02549; NID:q163617; PID:q163618  
 C:Genetics:  
 A:Gene: PRLR

Query Match 7.8%; Score 165; DB 2; Length 581;  
 Best Local Similarity 31.3%; Pred. No. 1.4e-05;  
 Matches 63; Conservative 24; Mismatches 96; Indels 18; Gaps 9;

QY 136 PFCAYQMDQCVYNNMOYLCSNKPFGIGVLDITNINNFYWEGLDHALOCVDYIKADGONI 195  
 DB 27 PPAKPKYVCRSPGKRTFCWMAEPGADGLPTNYTLTYHHEGETLLHECPDY-KTGGPN- 85  
 QY 195 GCAATPLEASDYDFYICVNGSENKPIRSSYFTFOLNIYKPLPPVYLFTFTRESSCEIK 255  
 DB 85 STYFGSKHYSIMKMYITVAINOMGSISSDPLVHVTYIVEPEPPANLLELKHEDRX 144  
 QY 256 ---LAKSIP-LGPAPCF--DYEIEIEDDTLVATVENET-YTLKTTN-ETROLCP 306  
 DB 145 PYIMIKSPPTMDVSGNFIIOYELRLKPERAT-----DWETHHTLQTOLEKINLY 198  
 QY 307 VVSLINIVICS-DDGIWSEWS 326  
 DB 199 GKYLVOIRCKPDHGYWSEWS 219

Search completed: January 19, 2000, 14:58:48  
 Job time: 3637 sec

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FT CARBOHYD 115 115 POTENTIAL.  
 FT CARBOHYD 215 215 POTENTIAL.  
 FT CARBOHYD 290 290 POTENTIAL.  
 FT CARBOHYD 299 299 POTENTIAL.  
 SQ SEQUENCE 380 AA: 44176 MW: 7254FFFA CRC32:

Query Match 100.0%; Score 2104; DB 1; Length 380;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-157;  
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATVCLAIIGLYFLISTFGCTSSSTETKVNPPDDEIVDPGYGLYLQWQPLSLD 60  
 DB 1 MATVCLAIIGLYFLISTFGCTSSSTETKVNPPDDEIVDPGYGLYLQWQPLSLD 60  
 QY 61 HFECEVEYELKRNIGSEWTKITITKNTLHYKGFPLDKNGEIKHTLLPWOCTNSSEVQ 120  
 DB 61 HFECEVEYELKRNIGSEWTKITITKNTLHYKGFPLDKNGEIKHTLLPWOCTNSSEVQ 120  
 QY 121 SSWAETTYWISPGIPEYKQVDMDCVYNNQYLLGSKMPGIGVLDNTNLFYWEGLDH 180  
 DB 121 SSWAETTYWISPGIPEYKQVDMDCVYNNQYLLGSKMPGIGVLDNTNLFYWEGLDH 180  
 QY 181 ALOCVYIRADGNICRPFYLLASDYKPYTCVNGSSSEKPIRSSYFTFOLQNIYKPLP 240  
 DB 181 ALOCVYIRADGNICRPFYLLASDYKPYTCVNGSSSEKPIRSSYFTFOLQNIYKPLP 240  
 QY 241 PVLVETRESSCEIKLWKSIPGLPAPRCFDEIEIREDDTTLVATVENEYTLKTNE 300  
 DB 241 PVLVETRESSCEIKLWKSIPGLPAPRCFDEIEIREDDTTLVATVENEYTLKTNE 300  
 QY 301 TRLCCEVNSKVNIVYSDGINSWSDKOCWEGEDISKRTLLRFLPFGFILLIVFVVG 360  
 DB 301 TRLCCEVNSKVNIVYSDGINSWSDKOCWEGEDISKRTLLRFLPFGFILLIVFVVG 360  
 QY 361 LLRKPNTPKMIPEFFCDT 380  
 DB 361 LLRKPNTPKMIPEFFCDT 380

RESULT 2  
 IL5R\_HUMAN STANDARD: PRT: 420 AA.  
 AC 001344:  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA) (CD125 ANTIGEN).  
 DE ANTI-GEN.  
 GN IL5RA OR IL5R.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 CC Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 92372031.  
 RA SCOTT H.S., GUO X.H., HOPWOOD J.J., MORRIS C.P.;  
 RT "Structure and sequence of the human alpha-L-iduronidase gene";  
 RL Genomics 13:1311-1313(1992).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 92357767.  
 RA TAVERNIER J., TYPENS T., PLAETINCK G., VERHEE A., FLEERS W.;  
 RT "Molecular basis of the membrane-anchored and two soluble isoforms of the human interleukin 5 receptor alpha subunit";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).  
 RN (3)  
 RP SEQUENCE OF 1-335 FROM N.A. (SI FORM).  
 RX MEDLINE: 92005669.  
 RA TAVERNIER J., DEVOS R., CORNELIS S., TYPENS T., VAN DER HEYDEN J.,  
 RA FLEERS W., PLAETINCK G.;  
 RT "A human high affinity interleukin-5 receptor (IL5R) is composed of

an IL5-specific alpha chain and a beta chain shared with the receptor for GM-CSF";  
 Cell 66:1175-1184(1991).  
 RL Cell 66:1175-1184(1991).  
 CC -1- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN BINDS TO IL-5.  
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: THREE ISOFORMS, TWO SOLUBLE FORMS AND A MEMBRANE-BOUND FORM EXIST DUE TO ALTERNATIVE SPLICING OF THE SAME GENE.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.  
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CDw125 entry;  
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw125.htm".  
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 CC EMBL: M96652; AAA59152.1;  
 DR EMBL: M96652; AAA59152.1;  
 DR EMBL: M78914; AAA36110.1;  
 DR EMBL: A26249; CA01793.1;  
 DR EMBL: A24587; CA01731.1;  
 DR EMBL: A26251; CA01794.1;  
 DR PIR: A40267; A40267.  
 DR MIM: 147851;  
 DR PROSITE: PS00241; RECEPTOR\_CYTOKINES\_1; FALSE NEG.  
 DR PROSITE: PS00340; RECEPTOR\_CYTOKINES\_2; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 420  
 FT DOMAIN 21 342  
 FT TRANSMEM 343 362  
 FT DOMAIN 363 420  
 FT CARBOHYD 35 35  
 FT CARBOHYD 131 131  
 FT CARBOHYD 216 216  
 FT CARBOHYD 244 244  
 FT CARBOHYD 333 335  
 FT CARBOHYD 336 420  
 FT CARBOHYD 333 333  
 FT CARBOHYD 334 420  
 FT CARBOHYD 420 AA: 47700 MW: 75C19847 CRC32;  
 SQ SEQUENCE

Query Match 14.88; Score 310.5; DB 1; Length 420;  
 Best Local Similarity 26.6%; Pred. No. 3.6e-17;  
 Matches 99; Conservative 70; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIKVNPDPDEFIVDPGYGLYLQWQPLSLDHRKECTVEELKRNIGSEWTKITIT 86  
 DB 25 DEKISLIPVNFITIKYTG-LAQVLLQWQPLSDPDEO-RNNVLEYOVINAPKREDDYETRT 82  
 QY 87 KNLHYKGFPLDKNGEIKHTLLPWOCTNSSEVSWAETTYWISPGIPEYKQVDMDCV 146  
 DB 83 ES-KCVTLHKGFSAVETILQ--NBSILASSMASEKLH-APGSPGISYVLTCT 135  
 QY 147 -----YYWQYLL-CSMKPGIGVLDNTNLFY-----WYEGLDHALOCVDYIKAD 191  
 DB 136 TWTEEDYNSLRKYOVSLRCTLVGDADPDYQFLYRYGSGWTE-----PCQERSKDT 189  
 QY 192 -GQNGCRFP--YLEADYKDPYICVNGSSSEKPIRSSYFTFOLQNIYKPLPVTFTFR 248  
 DB 190 LGNNIACWPFRTILSKGDMSLVYNGSSSKSALRPFOQLALHADIDINPLANTAEI 249  
 QY 249 ESSCEIKLWKSIPGLPAPRCFDEIEIREDDTTLVATVENEYTLKTNETROLCFV 308

DB 250 EGT-RLSIOMEPVSAFPIHCEYEVKIHNTNGVIOIEKLMNATISIIDLSKDYOV 308  
 QY 309 RSKVNYICDDGDSWMSKOCHEGDLRSKTLIRFWLPFGFLLIL-----VIFPTGLL 362  
 DB 309 RAAVSSMCHEAGLMSWS--QPIYGVNDEKRP--LREM---FVIVIMATICFILLISLI 361  
 QY 363 LRKNTYPMIP 374  
 DB 362 CKICHIMIKLPF 373

RESULT 3  
 ID 1131 MOUSE STANDARD: PRT: 424 AA.  
 AC 009030:  
 DT 01-NOV-1997 (rel. 35, Created)  
 DT 01-NOV-1997 (rel. 35, Last sequence update)  
 DE 15-JUL-1999 (rel. 38, Last annotation update)  
 DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-13RA-1) (INTERLEUKIN-13 BINDING PROTEIN) (NR4).  
 GN IL13RA1 OR IL13RA OR IL13R.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 96133964.  
 RA HILTON D.J., ZHANG J.-G., METCALF D., ALEXANDER W.S., NICOLA N.A., WILSON T.A.;  
 RT "Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).  
 CC -1- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY (BY SIMILARITY).  
 CC -1- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA, IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: SPLEEN, LIVER, THYMUS, HEART, LUNG, KIDNEY, TESTIS, STOMACH, BRAIN, SKIN, AND COLON; BUT NOT SKELETAL MUSCLE.  
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
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 CC EMBL: S80963; AAB50695.1;  
 DR MGI:105052; IL13RA.  
 DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.  
 FT SIGNAL 1 25  
 FT CHAIN 26 424  
 FT DOMAIN 26 340  
 FT TRANSMEM 341 364  
 FT DOMAIN 365 424  
 FT DOMAIN 37 100  
 FT DISULFID 44 93  
 FT DISULFID 132 142  
 FT DISULFID 171 183  
 FT CARBOHYD 35 35  
 FT CARBOHYD 59 59  
 FT CARBOHYD 103 103  
 FT CARBOHYD 136 136  
 FT CARBOHYD 262 262  
 FT CARBOHYD 338 338

SEQUENCE 424 AA: 48402 MW: 1115963 CRC32:  
 Query Match 14.2%; Score 298; DB 1; Length 424;  
 Best Local Similarity 25.8%; Pred. No. 3.5e-16;  
 Matches 108; Conservative 70; Mismatches 158; Indels 82; Gaps 21;  
 QY 8 IGLYFETVIST-TFGCTSSSDTEIKVNPPODEIYDPGLYGLYLQWOPPLS:CHKEECT 66  
 LK 7 LGELVLMLMTATVGVAAA--TEVQPPVTLNLSVENVLCITIMWSPPEGAS--PNCT 61  
 QY 67 VEX-----ELKRYNIGSETWKTITIKNLHYKDFGLINKGIEAKIHTLPWQCT-NGSEVQ 120  
 LK 62 LRYFSHIDQOQKIAPET-----HRKEELPDEKICIQVGS---QCSANESEKP 108  
 QY 121 SSNAEYVWIS-PQGLPERKVDMDQCVYNNQYLCSKMPGIGVLDITNINLFYWEGLD 179  
 D5 109 SPLVKRC--ISPEGQPEASVELKCIWHNLSYMKCSWLPGRNTSPDITLYLYWYSSLE 166  
 QY 180 HALQVDYIKADQONIGCFEPLDAS---DYKDFYICVNGSSEKPIRSSYTFPOLQNTY 236  
 LK 167 KSRQC-ENIYRQGHACFKLTKVEPSEHONVQIMVDMNAG--IRSCKIYSLTSYV 223  
 QY 237 KPI-PVYLFTFRESCEIKLWSTPLGPIPARCFDEIEIR----- 278  
 D5 224 KPDPF-PKHLKLLKNGALLVQWKNPNQ-PRSRCLTYEYEVNNTQDRHNILVEEDKQN 281  
 QY 278 -EDYITL-----VATVENEYITLKTNETRQLOCFYVRKVNICYSDGDMSEMSDQ 329  
 D5 222 SESDFEGETSCFQLPGVADAVYIVRVKTKLCE-----DNRKMSDMSDAQ 331  
 QY 330 CHEGDLRSKTLIRFWLPFGFLLILVIVTGLLR-KENYTP-----KMIPEFCD 379  
 D5 332 FSGPFGNSGFYITMLTIV-FVAHAVIILLIYKRLKIIIPPIPDPKIRKEMGD 388

RESULT 4  
 ID 1131 HUMAN STANDARD: PRT: 427 AA.  
 AC P78552: Q09656:  
 DT 01-NOV-1997 (rel. 35, Created)  
 DT 01-NOV-1997 (rel. 35, Last sequence update)  
 DE 15-JUL-1999 (rel. 38, Last annotation update)  
 DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-13PA-1).  
 GN IL13PA1 OR IL13RA OR IL13R.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE-CARCINOMA:  
 RX MEDLINE: 97165986.  
 RA WITOUX B., LAURENT P., BONNIN O., LUPKER J., CAPUT D., VITA N., FERRARA P.;  
 RT "Cloning of the human IL-13R alpha 1 chain and reconstitution with the IL13R alpha of a human IL-4/IL-13 receptor complex.";  
 RT FEBS Lett. 401:163-166(1997).  
 CC [2]  
 CC SEQUENCE FROM N.A.  
 CC TISSUE-B-CELL;  
 CC GAUCHAT J.F.M., SCHLAGENHAUF E., FENG N.-P., MOSER R., YAMAGI M., JEANIN P., AGUANI S., ELSON G., NOTARANGELO L.D., WELLS T., EUGSTER H. Z., BOURNEROT J.Y.;  
 CC Submitted (Jan-1997) to the EMBL/Genbank/DBJ databases.  
 CC [3]  
 CC SEQUENCE FROM N.A.  
 CC TISSUE-T-CELL;  
 CC MEDLINE: 97067184.  
 RA KIAN M.J., WAVEBI N., OBIRI N.I., PURI R.K., MODI W.S., LEONARD W.J.;  
 RT "cDNA cloning and characterization of the human interleukin 13 receptor alpha chain.";

```

RL J. Biol. Chem. 271:29265-29270(1996).
CC -1- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-
CC ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN
CC ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA
CC CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF
CC GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY.
CC -1- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA,
CC IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS IN HEART, LIVER,
CC SKELETAL MUSCLE AND OVARY; LOWEST LEVELS IN BRAIN, LUNG AND
CC KIDNEY. ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-slb.ch).
CC -----
DR EMBL: Y10659; CAA71669.1; -.
DR EMBL: Y09328; GAA70508.1; -.
DR EMBL: U62858; AAB37127.1; -.
DR HSSP: P31785; IILN.
DR MIM: 300119; -.
DR PFM: PF00041; fn3; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 21
FT CHAIN 22 427
FT DOMAIN 22 343
FT TRANSMEM 344 367
FT DOMAIN 368 427
FT DOMAIN 39 102
FT DISULFID 46 95
FT DISULFID 134 144
FT DISULFID 173 185
FT CARBOHYD 37 37
FT CARBOHYD 61 61
FT CARBOHYD 105 105
FT CARBOHYD 138 138
FT CARBOHYD 157 157
FT CARBOHYD 235 235
FT CARBOHYD 265 265
FT CARBOHYD 293 293
FT CARBOHYD 329 329
FT CARBOHYD 341 341
FT CONFLICT 130 130
FT CONFLICT 358 358
FT SEQUENCE 427 AA; 48759 MW; 88B33657 CRC32;

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|                           |        |                    |            |             |
|---------------------------|--------|--------------------|------------|-------------|
| Query Match               | 14.0%; | Score 295.5;       | DB 1;      | Length 427; |
| Best Local Similarity     | 26.0%; | Pred. No. 5.5e-16; |            |             |
| Matches 107; Conservative | 63;    | Mismatches 169;    | Indels 73; | Gaps 20     |

[illegible]

```

Db 173 C-ENIFRGQJEGGSFDLTIVKXDSFEQHSVQIWMKDNACKIKPSPFNIUPLTSRVADDP 231
Oy 242 --VILTFRESSCEIKLWSIPICPIRACDEDEIETREDDT-----LVITAVENET 233
Dc 232 HIKNLSFHN--DLYVOWENPQNF-I-RCILFEVNEVNSQTEHNVFYOEAKCENPE 287
Oy 234 TLKITTNEROLCFV-----RSKNVNYC-SDGSIMSEWSDKQWCEGSDSK 339
Db 288 ERNVENTS--CFWPGVLPDLTNTVIRIKYTNKLCEDEKLSMSNOE-----SIGKK 339
Oy 340 TLRRLWLPF-----GFIILVIFVTCG--TLRKPTYP-KMIPFEKCD 379
Db 340 RNSLTIVMLLIVPYIAGAIIVLLTLKRAKIIITPPIIDPGKIFEMEGCD 391

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## RESULT . 5

| ID | PLLR_CHICK | STANDARD; | PRT; | 831 AA. |
|----|------------|-----------|------|---------|
|----|------------|-----------|------|---------|

DT 01-JUN-1994 (Rel. 29, Created)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

GN PRLR.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;

RN [1]

RC STRAIN=WHITE LEGHORN; TISSUE=KIDNEY;  
EX REFERENCE=03075103

RA TANAKA M., MAEDA K., OKUBO T., NAKASHIMA K.;

|    |                            |                    |
|----|----------------------------|--------------------|
|    | RT , the cDNA sequence. "; |                    |
| rt | rt-PCR                     | 100 100 100 (3000) |

CC - FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE

CC-1: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN

CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS

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DR EMBL; D13154; .BAA02439.1; -  
DTP; T01655; T01655

DR. HSSP; P16471; 1BP3.  
DR. PEAM; PE00041. 4P3.

DR PROSITE; PS00241; R  
DQ PROSITE; P000340; R

| KW | Receptor; | Transmembrane; | Glycoprotein; | Signal; | Repeat |
|----|-----------|----------------|---------------|---------|--------|
| ET | 1         | 3              | 3             | 3       | 3      |

|    |        |    |     |                               |
|----|--------|----|-----|-------------------------------|
| ET | CHAIN  | 24 | 831 | PROLACTIN RECEPTOR.           |
| ET | DOMAIN | 24 | 439 | EXTRACTIVITY AND POTENTIALITY |

| ITEM | DESCRIPTION              | QTY | UNIT | PRICE | TOTAL |
|------|--------------------------|-----|------|-------|-------|
| 1    | POTENTIAL.               | 1   | EA   | 459   | 459   |
| 2    | TRANSMEM                 | 1   | EA   | 450   | 450   |
| 3    | DOMA IN                  | 1   | EA   | 831   | 831   |
| 4    | CVTODI ASMTC (POTENTIAL) | 1   | EA   | 831   | 831   |

|              |     |     |                       |
|--------------|-----|-----|-----------------------|
| ENT - DOMAIN | 25  | 122 | FIBRONECTIN TYPE-III. |
| ENT - DOMAIN | 133 | 325 | FIBRONECTIN TYPE-III  |

|    |        |     |     |                       |
|----|--------|-----|-----|-----------------------|
| EM | DOMAIN | 228 | 325 | FIBRONECTIN TYPE-III. |
| EM | DOMAIN | 228 | 438 | FIBRONECTIN TYPE-III  |

BY SIMILARITY.  
46  
36  
DISULFID  
ET.

|               | POTENTIAL. |  |
|---------------|------------|--|
| ET CARBOHYD . | 59         |  |
| ET CARBOHYD . | 61         |  |

| FT   | CARBOHYD | POTENTIAL. |
|------|----------|------------|
| 1.00 | 100      |            |
| 1.13 | 113      |            |

|             | POTENTIAL. |  |
|-------------|------------|--|
| ET CARBOHYD | 132        |  |
| ET CARBOHYD | 363        |  |



FT CARBOHYD 303 303 POTENTIAL.  
 FT CARBOHYD 315 315 POTENTIAL.  
 FT CARBOHYD 335 335 POTENTIAL.  
 SO SEQUENCE 831 AA; 94102 MM; B977BF07 CRC32;

Query Match 12.5%; Score 263; DB 1; Length 831;  
 Best Local Similarity 26.4%; Pred. No. 4.2e-13;  
 Matches 103; Conservative 58; Mismatches 183; Indels 46; Gaps 17;

QY 18 TTFCTSSDTEIKV--PPQDE---YDPG-----YLGTYLQWPPSL 59  
 DB 97 TTFNITVATNEIGSNSSDPQYDVATSIYQSPVNLLETKRANIMYLMAKSPPLA 156  
 QY 60 DHKECTEVELKRYNIGSEMTKTTIKNLHYDGFNDLNGIAKIHITLLPQCTNGSEV 119  
 DB 157 DASSNHLHYELKIRKEKEEMETI--SVGVPTCKIKIN--LNAGMKRYVQVCTLDPE 212  
 QY 120 QSSMAETTYWISFQG-IPEKTVQDMCVYVNMQYLLCSMRPGIGVLLDTNYNLFYWEGL 178  
 DB 213 WSMWSEERHILIPSGSPPEKPIIKCRSEKETFTQWMPGIDGHPNTYLLTSGKEGE 272  
 QY 179 DHALOCVDYIKADGONIGCRPYLEASDYKDYICVNGSEENKPISSYFTFOLQNIKP 238  
 DB 273 EGVYECEDPY-RTAGPN-SCYFDEKHTSFMTIYNTVATNEIGSNSSDPHYVDVYIYOP 330  
 QY 239 LPVYCTFRESCEIK---LKMS--IPGIPARCFDEVEIEIR---EDDTLVATFVEN 290  
 DB 331 DPEVNTLEKPIKRNKPIVLTWSPPLADVNSGMLTLEYELRLKPESEEMETTFVGO 390  
 QY 291 ET-YLTKTNETRQLCFVYRSKVNICYSD--GIWSEMSDKQCE--GEDLSKTLTRFWL 346  
 DB 391 QYQYKMFSLNPKKYY-----IQHKCPDHGSMSESENITQIPNDPRVMDI-VWI 443  
 QY 347 PPGFT--LILVTFVIGLLLRKPNTPKMP 374  
 DB 444 VLGVLSTLCLIMSTMVWLKGYRMIFMLP 473

## RESULT 6

IL5R\_MOUSE STANDARD: PRT: 415 AA.  
 ID IL5R\_MOUSE

AC 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 GN INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91092260.  
 RA TAKAKI S., TOMINAGA A., MITA S., SONODA E., YAMAGUCHI N.,  
 RA TAKATSU K.;  
 RT "Molecular cloning and expression of the murine interleukin-5  
 receptor."  
 RT EMBO J. 9:4367-4374(1990).  
 RL -1- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN  
 CC BINDS TO IL-5.  
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA  
 CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS. ALSO  
 CC ON B-CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.  
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CC EMBL D90205; BAA14231.1; -  
 DB 91R; S12357; S12357.  
 DB MGD: MGI:96558; IL5RA.  
 DB PROSITE: PS00241; RECEPTOR CYTOKINES\_1; FALSE\_NEG.  
 DB PROSITE: PS00340; RECEPTOR CYTOKINES\_2; 1.  
 DB Receptor; Transmembrane; Glycoprotein; Signal.  
 DB SIGNAL 1 17  
 FT CHAIN 18 415 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.  
 FT DOMAIN 18 339 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 340 361 POTENTIAL.  
 FT DOMAIN 362 415 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 134 152 BY SIMILARITY.  
 FT DISULFID 179 193 BY SIMILARITY.  
 FT CARBOHYD 32 32 POTENTIAL.  
 FT CARBOHYD 128 128 POTENTIAL.  
 FT CARBOHYD 213 213 POTENTIAL.  
 FT CARBOHYD 241 241 POTENTIAL.  
 SO SEQUENCE 415 AA; 46989 MM; 41SD6A67 CRC32;

Query Match 11.7%; Score 247; DB 1; Length 415;  
 Best Local Similarity 24.6%; Pred. No. 3.2e-12;  
 Matches 91; Conservative 70; Mismatches 151; Indels 58; Gaps 18;

QY 34 PPDFIVDPGVIGYLYLQWPPSLDHFRECTEVELKRYNIGSEMTKTTIKNLHYD 93  
 DB 29 PPNVETIKATG-LAQVLLHMDPNPQEQ--RHVDLEHYKINAPQEDVDTRKTES---KC 83  
 QY 94 GFLNKGIAKTIITLLPQCTNGSEVQSSMAETTYWISFQIGETFTVQDMCVYVNMQYLL 150  
 DB 84 VYPLHGFAPASVYTIK---SSHITLASSWVSAEL-KAPGSGISVNLCTCTHIVASS 139  
 QY 150 ---WQY-LCSMRPGIGVLLDTNYNLFYWEGLDHALOCVDYIK-ADGONIGCRFP- 201  
 DB 140 HTLRLRYQVSLNCTWLVGADAPEDTQYFLYLRGVLT--KQCEYRDALNRTACWFR 197  
 QY 201 -VLEASDYKDYICVNGSEENKPISSYFTFOLQNIKPLPYLLTTFRESCEIKLMS 259  
 DB 198 TETNSKGFEDLAVHINGSKRAIKRFDOLFSLAIDQVNPANVVEIEN--SLYIQWE 256  
 QY 260 IPEGPIARCFDEVEIEIRDD-----TTVATVENVNTYLLKTNERQLCFVY 308  
 DB 257 KPLSAPDPCFNEELKTYNTRKNGHIOKEKLINKFTSKIDVSTYSIQ-----V 305  
 QY 309 RSKVNIYCSDDGIWSEMSDKQCEGEDLSKTLTRFW---LPFGFLLILVFTGLLR 364  
 DB 306 KAAVSSPCRNKPGKWSGMS-QPIYVKE--RKLIVE-WHLIVLPTACPVILIT--SLICR 359  
 QY 365 KPNTYPRKMP 374  
 DB 360 VCHLWTRLP 369

## RESULT 7

ENK1A\_MELGA STANDARD: PRT: 831 AA.  
 ID ENK1A\_MELGA

AC 091094; 091091; 091092;  
 DT 31-NOV-1997 (Rel. 35, Created)  
 DT 31-NOV-1997 (Rel. 35, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 GN PROLACTIN RECEPTOR PRECURSOR (PRL-R) (TPRLR).  
 OS PRLR.  
 OS Melagris gallopavo (Common turkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;  
 OC Neognathae; Galliformes; Melagris; Melagris.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX FISSUE-KIDNEY.  
 RX MEDLINE: 97057891.

RA ZHOU J.F., ZADNORNY D., GUEMENE D., KUHNLEIN U.;  
 RT "Molecular cloning, tissue distribution, and expression of the  
 RT prolactin receptor during various reproductive states in Meleagris  
 RT gallinavo."  
 RL Biol. Reprod. 55:1081-1090(1996).  
 RN [2]  
 RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.  
 RC TISSUE-Ovary;  
 RA PLYTS G.R., YOUNG S.K., POSTER D.N., EL HALAMANI M.E.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 CC - FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE  
 CC PROLACTIN.  
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC - SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.  
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 CC  
 DR EMBL: U76587; AAB01544.1;  
 DR EMBL: U22947; AAA75038.1;  
 DR EMBL: U22924; AAA75039.1;  
 DR HSSP: P16471; 1BP3.  
 DR PFAM: PF00041; fn3; 4.  
 DR PROSITE: PS00241; RECEPTOR\_CYTOKINES\_1; 2.  
 DR PROSITE: PS00340; RECEPTOR\_CYTOKINES\_2; 2.  
 KW Receptor; Transmembrane; Glycoprotein; signal; Repeat.  
 FT SIGNAL 1 23  
 FT CHAIN 24 831  
 FT DOMAIN 24 438  
 FT TRANSSEM 439 459  
 FT DOMAIN 460 831  
 FT DOMAIN 25 122  
 FT DOMAIN 123 225  
 FT DOMAIN 228 325  
 FT DOMAIN 326 428  
 FT DISULFID 36 46  
 FT DISULFID 75 86  
 FT CARBOHYD 59 91  
 FT CARBOHYD 91 91  
 FT CARBOHYD 100 100  
 FT CARBOHYD 112 112  
 FT CARBOHYD 132 132  
 FT CARBOHYD 262 262  
 FT CARBOHYD 303 303  
 FT CARBOHYD 315 315  
 FT CARBOHYD 335 335  
 FT SEQUENCE 831 AA; 94394 MW; F8715C98 CRC32;  
 Query Match 11.3%; Score 238; DB 1; Length 831;  
 Best Local Similarity 26.18; Pred. No. 3.7e-11;  
 Matches 97; Conservative 53; Mismatches 178; Indels 44; Gaps 17;  
 18 TTEGCTSSDTEIKVY--PDQFE-----IVDPG-----YLGILYQWQPLSL 59  
 97 TTYNTVATNEIGSSNDPOVDVTSIVOPGSPVNLLETORANYIMYLAKMSPPLLA 156  
 60 DHFECEIYEELKYNISSEWTKITITNKHKDGFDMKGEAKIHTLLPQCGNSEV 119  
 157 DASSNHLHYELRLKPEKEEYV---PVGVOYCKIKNR--LNAQMRVYVOYRCMLDGE 212  
 120 QSSW-AETTYVSPGIGETKQVQDMCYVYNNQYLCSMKPGIGVLLDTNYNLFYWGSL 178  
 213 WSEMSERRILLISGLSPERKTIKCSPEKEFTCKMKKPGDGHPTNLYLLSKSGE 272  
 179 DHALQCVDIKADGONICRPPYLEASDYKDFYICVNGSSSEKPIRSSYTFQLONIYKP 238

DB 273 EQVECPDY-RTAGPN-SCYEDKKHTSFVTYNTYKATNEMGSSNDPBYVDYIVCP 330  
 QY 239 LPPLYLFTFESSESEIR-----LKWS-IPICPIRA--RCFYEIEIR-EDDTLYLVANEN 220  
 DB 331 DPPANVLELEKPKINRRPYMLTLWSPPLDVGSGWTLTLYELKPEESEMTEYVGO 390  
 QY 291 ET-YTLKTNETROLCPVNSKVNICYSD--GIWSEMSKQWE-GEELSKTLRLFWL 346  
 DY 391 QYQYKMSLNPGRKYI-----VQIHKPDHSGMSSESENTEIENDRYKMI-VWI 443  
 QY 347 PEGFILLIVTFV 358  
 DB 444 VLGVLSTLICI 455  
 RESULT 8  
 CYRG\_HUMAN STANDARD; PRT; 369 AA.  
 ID CYRG\_HUMAN  
 AC P31785;  
 DT 01-JUN-1993 (Rel. 26, Created)  
 DT 01-JUN-1993 (Rel. 26, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C) (INTERLEUKIN-  
 DE 2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64) (CD132 ANTIGEN).  
 GN IL2RG.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.  
 RC MEDLINE; 92335883.  
 RA TAKESHITA T., ASAO H., OHTANI K., ISHII N., KUMAKI S., TANAKA N.,  
 RA MINAKATA H., NAKAMURA M., SUGAMURA K.;  
 RT "Cloning of the gamma chain of the human IL-2 receptor."  
 RL Science 257:379-382(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-LIVER.  
 RX MEDLINE; 93293887.  
 RA NOGUCHI M., ADELSTEIN S., CAO X., LEONARD W.J.;  
 RT "Characterization of the human interleukin-2 receptor gamma chain  
 RT gene."  
 RL J. Biol. Chem. 268:13601-13608(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A. AND VARIANTS ASP-114 AND ASN-153.  
 RX MEDLINE; 94004847.  
 RA PUCK J.M., DESCHENES S.M., PORTER J.C., DUTRA A.S., BROWN C.J.,  
 RA WILLARD H., HENTHORN P.S.;  
 RT "The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated  
 RT in X-linked severe combined immunodeficiency, SCIDX1."  
 RL Hum. Mol. Genet. 2:1099-1104(1993).  
 RN [4]  
 RP IDENTIFICATION AS A IL-4R SUBUNIT.  
 RX MEDLINE; 94090315.  
 RA KONDO M., TAKESHITA T., ISHII N., NAKAMURA M., WATANABE S.,  
 RA ARAI K.-I., SUGAMURA K.;  
 RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between  
 RT receptors for IL-2 and IL-4."  
 RL Science 262:1874-1877(1993).  
 RN [5]  
 RP IDENTIFICATION AS A IL-4R SUBUNIT.  
 RX MEDLINE; 94090317.  
 RA RUSSELL S.M., KREGAN A.D., HARADA N., NOGUCHI M.,  
 RA LELAND P., FRIEDMANN M.C., MIYAJIMA A., PURI R.K., PAUL W.E.,  
 RA LEONARD W.J.;  
 RT "Interleukin-2 receptor gamma chain: a functional component of the  
 RT interleukin-4 receptor."  
 RL Science 262:1880-1883(1993).  
 RN [6]  
 RP IDENTIFICATION AS A IL-7R SUBUNIT.  
 RX MEDLINE; 94090316.  
 RA NOGUCHI M., NAKAMURA Y., RUSSELL S.M., ZIEGLER S.F., TSANG M., CAO X.,  
 RA LEONARD W.J.;

RT "Interleukin-2 receptor gamma chain: a functional component of the  
 RT Interleukin-7 receptor";  
 RL Science 262:1877-1880(1993).  
 RN [17]  
 RP 3D-STRUCTURE MODELING OF 57-248.  
 RX MEDLINE; 95111955.  
 RA BAMBOURGH P., HEGGECOCK C.J., RICHARDS W.G.;  
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular  
 RT modelling";  
 RL Structure 2:839-851(1994).  
 RN [8]  
 RP VARIANTS XSCID PHE-115; CYS-240 AND ILE-241.  
 RX MEDLINE; 94130970.  
 RA DISANTO J.P., DAUTRY-VARSAT A., CERTAIN S., FISCHER A.,  
 RA DE SAINT BASILE G.;  
 RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked  
 RT severe combined immunodeficiency disease result in the loss of  
 RT high-affinity IL-2 receptor binding";  
 RL Eur. J. Immunol. 24:475-479(1994).  
 RN [9]  
 RP VARIANT XSCID LYS-68.  
 RX MEDLINE; 94375038.  
 RA MARIENWICZ S., SOBETIL A., DAUTRY-VARSAT A., FISCHER A.,  
 RA DE SAINT BASILE G.;  
 RT "Detection of three nonsense mutations and one missense mutation in  
 RT the interleukin-2 receptor gamma chain gene in SCIDx1 that  
 RT differently affect the mRNA processing";  
 RL Genomics 21:291-293(1994).  
 RN [10]  
 RP VARIANT XSCID HIS-162.  
 RX MEDLINE; 94300093.  
 RA ISHII N., ASAO H., KIMURA Y., TAKESHITA T., NAKAMURA M., TSUCHIYA S.,  
 RA KONNO T., MAEDA M., UCHIYAMA T., SUGAWARA K.;  
 RT "Impairment of ligand binding and growth signaling of mutant IL-2  
 RT receptor gamma-chains in patients with X-linked severe combined  
 RT immunodeficiency";  
 RL J. Immunol. 153:1310-1317(1994).  
 RN [11]  
 RP VARIANT XSCID ASN-39.  
 RX MEDLINE; 95023932.  
 RA DISANTO J.P., RIEUX-LAUCAT F., DAUTRY-VARSAT A., FISCHER A.,  
 RA DE SAINT BASILE G.;  
 RT "Defective human interleukin 2 receptor gamma chain in an atypical X  
 RT chromosome-linked severe combined immunodeficiency with peripheral T  
 RT cells";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470(1994).  
 RN [12]  
 RP VARIANTS XSCID CYS-226 AND HIS-226.  
 RX MEDLINE; 95397841.  
 RA PEPPER A.E., BUCKLEY R.H., SMALL T.N., PUCK J.M.;  
 RT "Two interlueon hotspots in the interleukin-2 receptor gamma chain  
 RT gene causing human X-linked severe combined immunodeficiency";  
 RL Am. J. Hum. Genet. 57:564-571(1995).  
 RN [13]  
 RP VARIANT XSCID SER-183.  
 RX MEDLINE; 96013903.  
 RA CLARK P.A., LESTER T., GENEY S., JONES A.M., HENDRIKS R.,  
 RA LEVINSKY R.L., KINNON C.;  
 RT "Screening for mutations causing X-linked severe combined  
 RT immunodeficiency in the IL-2R gamma chain gene by single-strand  
 RT conformation polymorphism analysis";  
 RL Hum. Genet. 96:427-432(1995).  
 RN [14]  
 RP VARIANT XSCID GLN-HIS-TRP INS-237.  
 RX MEDLINE; 95164726.  
 RA PUCK J.M., PEPPER A.E., BEDARD P.M., LAFRANCOISE R.;  
 RT "Female germ line mosaicism as the origin of a unique  
 RT gamma-chain mutation causing X-linked severe combined  
 RT immunodeficiency";  
 RL J. Clin. Invest. 95:895-899(1995).  
 RN [15]  
 RP VARIANT XSCID GLN-271.  
 RX MEDLINE; 95190013.

RA SCHNALETTIG F.C., LEONARD W.J., NOGUCHI M., BERG M., RUDLOFF H.E.,  
 RA DENNEY R.F., DAVE S.R., BROOKS E.G., GOLDMAN A.S.;  
 RT "Missense mutation in exon 7 of the common gamma chain gene causes a  
 RT moderate form of X-linked combined immunodeficiency";  
 RL J. Clin. Invest. 95:1169-1173(1995).  
 RN [16]  
 RP VARIANT XSCID ARG-115.  
 RX MEDLINE; 97042245.  
 RA STEPHAN V., MAHN V., LE DEIST F., DIRKSEN U., BROKER B.,  
 RA MULLER-FLECKENSTEIN I., HORNEFF G., SCHROTEN H., FISCHER A.,  
 RA DE SAINT BASILE G.;  
 RT "Atypical X-linked severe combined immunodeficiency due to possible  
 RT spontaneous reversion of the genetic defect in T cells";  
 RL New Engl. J. Med. 335:1563-1567(1996).  
 RN [17]  
 RP VARIANT XSCID GLN-285.  
 RX MEDLINE; 97295088.  
 RA JONES A.M., CLARK P.A., KATZ F., GENEY S., MCMAHON C., ALTERNAN L.,  
 RA CANT A., KINNON C.;  
 RT "B-cell-negative severe combined immunodeficiency associated with a  
 RT common gamma chain mutation";  
 RL Hum. Genet. 99:677-680(1997).  
 RN [18]  
 RP VARIANT XSCID CYS-222.  
 RX MEDLINE; 98064061.  
 RA SHARPE N., SHAHAR M., ROIFMAN C.M.;  
 RT "An interleukin-2 receptor gamma chain mutation with normal thymus  
 RT morphology";  
 RL J. Clin. Invest. 100:3036-3043(1997).  
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF  
 CC INTERLEUKINS.  
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND  
 CC PROBABLY ALSO THE IL-13 RECEPTORS.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED  
 CC IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMMAGLOBULINEMIA, SWISS TYPE  
 CC OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- DATABASE: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide cd132 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd132.htm".  
 CC -1- DATABASE: NAME-IL2RGbase; NOTE-X-linked SCID mutation database;  
 CC WWW="http://www.nhgri.nih.gov/DIR/LGT/SCID/IL2RGbase.html".  
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 DR EMBL; D11085; BAA01857.1;  
 DR EMBL; I12183; AAA59145.1;  
 DR EMBL; I12178; AAA59145.1; JOINED.  
 DR EMBL; I12176; AAA59145.1; JOINED.  
 DR EMBL; I12177; AAA59145.1; JOINED.  
 DR EMBL; I12179; AAA59145.1; JOINED.  
 DR EMBL; I12180; AAA59145.1; JOINED.  
 DR EMBL; I12181; AAA59145.1; JOINED.  
 DR EMBL; I12182; AAA59145.1; JOINED.  
 DR EMBL; I19546; AAC37524.1;  
 DR PIR; A42565; A42565.  
 DR PDB; 1TLM; 26-JAN-95.  
 DR QDB; 1TLM; 26-JAN-95.  
 DR KIM; 300400;  
 DR KIM; 308380;  
 DR JFM; PF00041; fn3: 1.  
 DR PROSITE; PS00041; RECEPTOR\_CYTOKINES\_1;  
 DR PROSITE; PS00340; RECEPTOR\_CYTOKINES\_2; FALSE\_NEG.  
 DR Receptor; Transmembrane; Glycoprotein; Signal; Disease mutation;  
 Query Match 10.5%; Score 220; DB 1; Length 369;



```

RT RT "Characterization of cDNAs encoding the murine interleukin 2 receptor
RT RT IL-2R gamma chain: chromosomal mapping and tissue specificity of
RT RT IL-2R gamma chain expression.";
RT RL Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).
RN RN [3]
RN RN SEQUENCE FROM N.A.
RX RX MEDLINE: 93366191.
RA RA KOBAYASHI N., NAKAGAWA S., MINAMI Y., TANIGUCHI T., KONO T.:
RT RT "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
RT RT gamma.";
RN RN Gene 130:303-304(1993).
RN RN [4]
RN RN SEQUENCE FROM N.A.
RX RX MEDLINE: 95104285.
RA RA DISANTO J.P., CERTAIN S., WILSON A., MACDONALD H.R., AVNER P.,
RA RA FISCHER A., DE SAINT BASILE G.:
RT RT "The murine interleukin-2 receptor gamma chain gene: organization,
RT RT chromosomal localization and expression in the adult thymus.";
RN RN Eur. J. Immunol. 24:3014-3018(1994).
RN RN [5]
RN RN SEQUENCE FROM N.A.
RP RP STRAIN-B6.S;
RX RX MEDLINE: 96341745.
RA RA CHIU R.K., DROLL A., COOPER D.L., DOUGHERTY S.T., DIRKS J.F.,
RA RA DOUGHERTY G.J.:
RT RT "Molecular mechanisms regulating the hyaluronan binding activity of
RT RT the adhesion protein CD44.";
RL RL J. Neurooncol. 26:231-239(1995).
CC CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC CC INTERLEUKINS.
CC CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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CC CC or send an email to license@sib-sib.ch).
CC CC -----
DR DR EMBL: D13821: BAA02974.1; -
DR DR EMBL: U21795: AAA64279.1; -
DR DR EMBL: D13565: BAA02760.1; -
DR DR EMBL: L20048: AAA39286.1; -
DR DR EMBL: S75852: AAB32904.1; -
DR DR EMBL: S75844: AAB32904.1; JOINED.
DR DR EMBL: S75845: AAB32904.1; JOINED.
DR DR EMBL: S75847: AAB32904.1; JOINED.
DR DR EMBL: S75848: AAB32904.1; JOINED.
DR DR EMBL: S75849: AAB32904.1; JOINED.
DR DR EMBL: S75850: AAB32904.1; JOINED.
DR DR EMBL: S75851: AAB32904.1; JOINED.
DR DR EMBL: X75337: CAA53085.1; -
DR DR PIR: JN0592: JN0592.
DR DR PIR: JN0775: JN0775.
DR DR HSSP: P31785: IILN.
DR DR MGD: MGI:96551; IL2RG.
DR DR PFM: PFM0044; fn3; 1.
DR DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
DR DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; FALSE_NEG.
KW KW Receptor; Transmembrane; Glycoprotein; signal.
FT FT SIGNAL 1 22
FT FT CHAIN 23 369
FT FT DOMAIN 23 263
FT FT TRANSMEM 264 284
FT FT DOMAIN 285 369
FT FT DOMAIN 151 250
FT FT DISULFID 62 72
FT FT DISULFID 102 115
FT FT POTENTIAL.

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FF CARBOHYD 71 71 POTENTIAL.
EE CARBOHYD 75 75 POTENTIAL.
FT CARBOHYD 84 84 POTENTIAL.
FU CARBOHYD 96 96 POTENTIAL.
FF CARBOHYD 159 159 POTENTIAL.
FT CARBOHYD 164 164 POTENTIAL.
S1 SEQUENCE 369 AA; 42241 MW; 60230FE27 CRC32;

Query Match 10.18; Score 212.5; DB 1; Length 369;
Jest Local Similarity 26.98; Pred. No. 1.36-09;
Matches 67; Conservative 43; Mismatches 116; Indels 23; Gaps 9;

QY 136 PETKQNDQDCYYNNQYLLCSN----KRGIGVLDNTNLTFTYEGDLHAL--QCVDIK 189
Dy 53 FTLPLPEVQCEVFNEYNMCTWNSSESOA-----TNTLTLYRYKVSNNNFQECSHYLF 107
QY 190 ADGQIGRFRPLYEASDKKDFYICVNGSSFNKPRSSFTFQLOINIVLDPVLYLTFRRE 249
Db 108 SKETSGGQIOKEDQLQYTFVVL--ODPQPPORRAQKLNLOLVLPAPENLTLSNL 165
QY 253 SSLEKLMKWSIPLGIPARCFDEIEIRED-DTTLVATVENS--TYLTKTNETRQLCFV 307
Db 156 SESQLEFLMK--SRIKRKRCLOLYLVQYSNDRSKTELVNHEPFLSPYDELKRYTRF 223
QY 308 VRSKAVNYICSDGGITWSEMSKQCWEG---EDLSKTLRLRWLPGRF--ILIVLFTVGL 361
Dy 224 VRSRNPICSSSQMSKQSPVHMGSHTVEENPSLFAEVLIPVGTGLITLTFVYCW 283
QY 362 LLRKNTYP 370
Dy 284 LERMEPIPP 292

RESULT 11
CYRG_CANFA STANDARD; PRT; 373 AA.
AC P40321;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUDIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (p64).
GN IL2RG.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RS SEQUENCE FROM N.A.
FU TISSUE-SPLEEN;
RC MEDLINE; 95130114.
RA HENTHORN P.S., SOMEERG R.L., FIMIANI V.M., PUCK J.M., PATTERSON D.F.,
RA KETLSBURG P.J.;
RA "IL-2R gamma gene microdeletion demonstrates that canine X-linked
RA severe combined immunodeficiency is a homologue of the human
RA disease.";
RL Genomics 23:69-74(1994).
CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED
CC SEVERE COMBINED IMMUNODEFICIENCY.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBROECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC -----  
DR EMBL; U04361; AAC48403.1;  
DR HSSP; P31785; 11LN.  
DR PFAM; PF00041; fn3; 1.  
DR PROSITE; PS00241; RECEPTOR\_CYTOKINES\_1; 1.  
DR PROSITE; PS00340; RECEPTOR\_CYTOKINES\_2; FALSE.NEG.  
DR PROSITE; PS00340; RECEPTOR\_CYTOKINES\_2; 1.  
KW Receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 373  
FT DOMAIN 23 261  
FT TRANSEM 262 283  
FT DOMAIN 284 373  
FT DOMAIN 151 249  
FT DISULFID 62 72  
FT DISULFID 102 115  
FT CARBOHYD 24 24  
FT CARBOHYD 71 71  
FT CARBOHYD 75 75  
FT CARBOHYD 84 84  
FT CARBOHYD 159 159  
FT CARBOHYD 164 164  
FT CARBOHYD 249 249  
SQ SEQUENCE 373 AA; 42516 MW; 6FD817E0 CRC32;

Query Match 9.9%; Score 208; DB 1; Length 373;  
Best Local Similarity 26.0%; Pred. No. 3e-09;  
Matches 69; Conservative 48; Mismatches 108; Indels 40; Gaps 12;

QY 115 NGSE-----VQSSAETTWISPOGIPETKVQDMCVYIMWYLLCSW-----KFGI 161  
DB 31 NGNEDIDPDEFLLTAPSET---LSVSSLPLEVO---CFEVEVEVMNCTMNSSEPRP-- 83  
QY 162 GVLLDTNNTNLYWYEGGL--DHALOCVDYIKADGQNGICRFPYLESDVKDFICNGSSE 219  
DB 83 -----TNLTLYWYKNSMDNDVQECGHYLFSEVTAGCMLQKEETHLYETEVYQVLDPRE 137  
QY 220 NKPIRSSYFTOLONIYVLPVYLYFTRESSCEIKLWMSIPLGIPARCEDEYEIEIRD 279  
DB 138 --PROSTQKLOLVIPWAPENITLNLSSQLELMS--NNHLDHGLEHVQYKSD 192  
QY 280 -DTLVATVEN-ETYLKTNETROLCFVYRSKVNITCSDDGISEMSDKOCWGEDLS 337  
DB 193 WDRSWTEQSVDRHSFSLPSVDGQGFYFRVRSRNPCLGSKQMSWSPHIM--GSNTS 251  
QY 338 KKTLL---RFLMPFGFLLIVIFV 358  
DB 252 KENPLFASAVLIPGSMGLIISLI 276

RESULT 12  
IL3B MOUSE STANDARD: PRT: 878 AA.  
AC P26954;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE INTERLEUKIN-3 RECEPTOR CLASS II BETA CHAIN PRECURSOR.  
GN AT2CA OR IL3RB2 OR IL3R.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 90117145.  
RA ITOH N., YONEHARA S., SCHREURS J., GORMAN D.M., MARUTAMA K., ISHII A.,  
RA YAHARA I., ARAI K., MIYAJIMA A.;  
RT Cloning of an interleukin-3 receptor gene: a member of a distinct  
RT receptor gene family.  
RL Science 247:324-327(1990).  
CC -!- FUNCTION: IN MOUSE THERE ARE TWO CLASSES OF HIGH-AFFINITY IL-3  
RECEPTORS. ONE CONTAINS THIS IL-3-SPECIFIC BETA CHAIN AND THE

OTHER CONTAINS THE BETA CHAIN ALSO SHARED BY HIGH-AFFINITY IL-5  
AND GM-CSF RECEPTORS.  
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
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DR EMBL; M29855; AAA39295.1;  
DR PIR; A40091; A40091.  
DR MGD; MGI:96555; IL3RB2.  
DR PFAM; PF00041; fn3; 2.  
DR PROSITE; PS00241; RECEPTOR\_CYTOKINES\_1; 1.  
DR PROSITE; PS00340; RECEPTOR\_CYTOKINES\_2; 1.  
KW Receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 878  
FT DOMAIN 23 440  
FT TRANSEM 441 462  
FT DOMAIN 463 878  
FT DISULFID 39 49  
FT DISULFID 78 95  
FT DISULFID 254 264  
FT DISULFID 293 310  
FT CARBOHYD 62 62  
FT CARBOHYD 350 350  
SQ SEQUENCE 878 AA; 97195 MW; 11C35BF CRC32;

Query Match 9.3%; Score 195; DB 1; Length 878;  
Best Local Similarity 24.1%; Pred. No. 8.8e-08;  
Matches 86; Conservative 59; Mismatches 150; Indels 62; Gaps 23;

QY 34 PRODFEYDPIGLYLYQWQPL---SLDFKCYEYELKYNISSEWTKITITNKLH 90  
DB 139 PKDIIHSPSG--DHFLLEWVSIGDSQVSWLSKDIIEFVAYKRL--QDSMED--ASSLH 193  
QY 91 YKDFDLKKGIEAKIHITLP-----WQCTNGSEVQ---SSMAETTWISPOGIPET 138  
DB 194 -TSNFQVH--LEPL--FLPNSITAAKRTIRLSAGSSISGRPSWSEVHWDSPG--DKA 247  
QY 139 KVQDMDCVYIMWYLLCSWKPGLGVLLDTNNTNLYWYEGGLDHALOCVDYIKADGQNT--- 196  
DB 248 QPNLQCFEFGDQSLHCSWEMVWTQTSVSFGFLFRSPAPAEKCSPVYKPEASVYTR 307  
QY 196 -GCRFYLEASDYKDFYICVNGSSEKPIRSSYFTFOLQNIYVLPVY--LTFRESSCE 253  
DB 308 YRCSLPVPEPSAHQYIVSYVHLEQKFI--MSYHIQME-----PILNQTKNRDS--- 358  
QY 254 IKLWMSIPLGIPARCPD--YEIEIRDDTLVATVEN-----ETYLKTNETROLCFV 307  
DB 358 YSLWETQKIT--KYIDHFFQVYKKKSESWKSKLENAGRNVSMDLPQLEPDTSYCAR 414  
QY 308 VRSK-VNLYCSDGIGWSEMSDKOCWGEDLSKKTLLRFPFGFLLIVFVTCGLL 363  
DB 415 VRVAPISDY--DQIWSEMSNEYTWI--TDWVMPRL---WI-----VLLVLELIFILL 460

RESULT 13  
CYRG\_BOVIN STANDARD: PRT: 379 AA.  
AC Q95118;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1998 (Rel. 35, Last annotation update)  
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)

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DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96268473.
RA YOO J., STONE R.T., SOLINAS-TOLDO S., FRIES R., BEATTIE C.W.;
RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor
RT gamma gene.";
RL DNA Cell Biol. 15:453-459(1996);
CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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CC -----
DR EMBL: U33748; AAB07812.1; -.
DR HSSP: P31785; 1ILN.
DR PFAM: PF00041; fn3: 1.
DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; FALSE_NEG.
RW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 379 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT DOMAIN 23 269 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 270 290 POTENTIAL.
FT DOMAIN 291 379 CYTOPLASMIC (POTENTIAL).
FT DISULFID 68 78 FIBRONECTIN TYPE-III.
FT DISULFID 109 122 POTENTIAL.
FT CARBOHYD 77 77 POTENTIAL.
FT CARBOHYD 81 81 POTENTIAL.
FT CARBOHYD 90 90 POTENTIAL.
FT CARBOHYD 166 166 POTENTIAL.
FT CARBOHYD 171 171 POTENTIAL.
SQ SEQUENCE 379 AA; 43037 MW; 52EF5D72 CRC32;

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1 CTRB..HUMAN STANDARD: PRT: 897 AA.
2 ID CYBB HUMAN P32927.
3 SC 01-OCT-1993 (Rel. 27, Created)
4 ST 01-FEB-1998 (Rel. 33, Last sequence update)
5 DT 01-NOV-1997 (Rel. 35, Last annotation update)
6 DE CYTOKINE RECEPTOR COMMON BETA CHAIN PRECURSOR (CD131 ANTIGEN).
7 NE CSF2PB OR IL3RB OR IL3RB.
8 GV Homo sapiens (Human).
9 CS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
10 CC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
11 [1]
12 FP SEQUENCE FROM N.A.
13 FM MEDLINE: 91088571.
14 RX HAYASHIDA K., KITAMURA T., GORMAN D.M., ARAI K., YOKOTA T.,
15 RA MITAJIMA A.
16 RT "Molecular cloning of a second subunit of the receptor for human
17 RY granulocyte-macrophage colony-stimulating factor (GM-CSF):
18 FT reconstitution of a high-affinity GM-CSF receptor."
19 FT Proc Natl. Acad. Sci. U.S.A. 87:9655-9659(1990).
20 [2]
21 R4 REVISION TO 454.
22 R5 KITAMURA T.
23 RA Submitted (FEB-1991) to the EMBL/GenBank/DBJ databases.
24 CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5
25 CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
26 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
27 CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
28 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
29 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
30 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
31 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CDw131 entry;
32 CC WWW: http://www.ncbi.nlm.nih.gov/prow/cd/cdw131.htm.
33 CC -
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41 CC -
42 DR EMBL; M59841; AAA18171.1; -
43 DR PIR; A39285; A39285.
44 DR FFM; PF00041; fn3; 2.
45 DR MIM; 138981; -
46 DR PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 2.
47 DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
48 KK Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
49 FT SIGNAL 1
50 FT CHAIN 16
51 FT SIGNAL 17
52 FT CHAIN 17
53 FT DOMAIN 17 897
54 FT TRANSMEM 17 443
55 FT TRANSMEM 17 460
56 FT DOMAIN 129 387
57 FT DOMAIN 336 434
58 FT DISULFID 35 45
59 FT DISULFID 75 91
60 FT CARBOHYD 58 58
61 FT CARBOHYD 191
62 FT CARBOHYD 346
63 SQ SEQUENCE 897 AA; 97335 MW; AC43EAS5 CRC32;
64
65 Query Match 8.5%; Score 178.5; DB 1; Length 897;
66 3rd Local Similarity 22.5%; Pred. No. 1.7e-06;
67 Matches 89; Conservative 57; Mismatches 144; Indels 105; Gaps 21.
68
69 32 VNPDPFEIVPGYGLY-----TYLQKQP-----LSLDF----- 63
70 97 VLPQSFVYVDYDYSFQDPRLGLRLVTLQHQPFEPRLQISTDDHLLTWSVAL 156
71
72 63 -----KCTVEYELRYRNIGSETWK--TITIKNLHYKQDFLNGKIE-----A 103

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|    |          |         |          |                       |
|----|----------|---------|----------|-----------------------|
| FT | DOMAIN   | 132     | 241      | FIBRONECTIN TYPE-III. |
| FT | DOMAIN   | 343     | 440      | FIBRONECTIN TYPE-III. |
| FT | DISULFID | 39      | 49       | BY SIMILARITY.        |
| FT | DISULFID | 77      | 94       | BY SIMILARITY.        |
| FT | CARBOHYD | 62      | 62       | POTENTIAL.            |
| FT | CARBOHYD | 141     | 141      | POTENTIAL.            |
| FT | CARBOHYD | 350     | 350      | POTENTIAL.            |
| SO | SEQUENCE | 896 AA; | 9911 MM; | AA906051 CRC32;       |

Query Match 8.2%; Score 173.5; DB 1; Length 896;  
Best Local Similarity 20.7%; Pred. No. 4.3e-06;  
Matches 81; Conservative 69; Mismatches 185; Indels 57; Gaps

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| Oy | 5   | CLAIGCLTEFLISTTGGTS-----SSPTER-----VNPPQDEIYDPGLGY           | 48  |
| Db | 94  | CVPRCVCPY---TRFSTTNDYYSFRPDSQGLWPLAQNQVPLPKNVSISSEDR         | 156 |
| Oy | 49  | LYLOMOPPL---SLDHKECVVEYELKRNKSGEYTKWTIITKN-----LHKDGFNDKNG   | 100 |
| Db | 151 | FLLEKSVSLGNAQVSWLSKRIEYVAKKRL-QDSWEDAYSLSHKRQVNEERPLFLPNS    | 205 |
| Oy | 101 | IEA-KIHT-LLPWOCTNGSEVOSSMAETTYTISPQGIPETRKQVDMDCVYYNWOYLCSWK | 156 |
| Db | 210 | IYAPVRFRLRXPSSLSGR--PSRMSPEAHWDSPQ-DKAPQNIQCFDGIQSLHCSWE     | 266 |
| Oy | 159 | PGIYGLDTNNLTNYWYEGDLHAQCYDYIK-AQONI-----GGRFYLEADSKDYIC      | 213 |
| Db | 267 | VMTQTGTSVSGLEGRDPSPAPEKCSGVNAEPGASVYTRYHCSLVPPEPSAHSQYTVS    | 328 |
| Oy | 214 | VNGSSENPPIRSSYFTFOLQNIVRKLPDPVYLTFFRESSECIKLWSIPLGIPARCFDYE  | 273 |
| Db | 327 | V-----KHLQGRFMSYNIIQMEPPLNITKNRDS---YSLMEWQKMAYSRIEHTFQ      | 377 |
| Oy | 274 | IEIREDDTLYTAIVEN--EYTLKTTNTRQLOCFVVRSKYNIYCSDDGIWSEMSQOCW    | 331 |
| Db | 378 | VOYKKKSDSWEDSSTENIDRAHSMDLSQLPEPDSYCARAVRKPISNYDGIWMSKSEYTW  | 437 |
| Oy | 332 | EGEDLSKTKTLRFLPGLPGFILLIYFTGILL                              | 363 |
| Db | 438 | K-TDWVPEFL--WI-----VILVFLIITILL                              | 461 |



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 20, 2000, 06:21:02 ; Search time 24.34 Seconds  
(without alignments)  
956.326 Million cell updates/sec

```

Title: US-09-077-817-2
Perfect score: 2104
Sequence: 1 MAFVCLAIGCLYTFELISTTF.....LLRKPNTPYKMIPEFCDT 380

```

Scoring table: BLOSUM62

Searched: 199794 seqs, 61255205 residues

Database : SPTREMBL\_11:\*

word size : 0

Number of hits that pass the threshold : 199794

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_omni:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_protein:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*

**Pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

| Result | Query  | Match | Length | DB | ID      | Description                   |
|--------|--------|-------|--------|----|---------|-------------------------------|
| No.    | Score  |       |        |    |         |                               |
| 1      | 1194.5 | 56.8  | 383    | 11 | 088786  | 088786 mus musculus           |
| 2      | 311.5  | 14.8  | 420    | 4  | Q14633  | Q14633 homo sapien            |
| 3      | 310.5  | 14.8  | 396    | 4  | Q14631  | Q14631 homo sapien            |
| 4      | 298.5  | 14.2  | 415    | 11 | 092004  | 092004 cavia porcea           |
| 5      | 292    | 13.9  | 333    | 4  | Q15469  | Q15469 homo sapien            |
| 6      | 291.5  | 13.9  | 427    | 4  | Q095646 | Q095646 homo sapien           |
| 7      | 264.5  | 12.6  | 349    | 6  | Q097597 | Q097597 bos taurus            |
| 8      | 178    | 8.5   | 896    | 11 | 064146  | 064146 rattus norvegicus      |
| 9      | 173.5  | 8.2   | 881    | 13 | 057519  | 057519 xenopus laevis         |
| 10     | 170    | 8.1   | 890    | 11 | Q92160  | Q92160 cavia porcea           |
| 11     | 165    | 7.8   | 296    | 6  | Q18880  | Q18880 bos taurus             |
| 12     | 159    | 7.6   | 581    | 6  | Q46561  | Q46561 ovis aries             |
| 13     | 153    | 7.3   | 217    | 6  | Q46386  | Q46386 mustela vison          |
| 14     | 151    | 7.2   | 862    | 4  | Q09665  | Q09665 homo sapien            |
| 15     | 151    | 7.2   | 206    | 4  | Q16354  | Q16354 homo sapien            |
| 16     | 145.5  | 6.9   | 420    | 4  | Q075462 | Q075462 homo sapien           |
| 17     | 142.5  | 6.8   | 412    | 4  | Q14431  | Q14431 homo sapien            |
| 18     | 135    | 6.4   | 346    | 13 | Q093404 | Q093404 oreochromis niloticus |
| 19     | 133.5  | 6.3   | 333    | 3  | Q15564  | Q15564 homo sapien            |
| 20     | 130.5  | 6.2   | 198    | 6  | Q18985  | Q18985 cervus elaphus         |
| 21     | 128    | 6.1   | 874    | 11 | P97378  | P97378 mus musculus           |
| 22     | 117.5  | 5.6   | 958    | 4  | Q13592  | Q13592 homo sapien            |
| 23     | 117.5  | 5.6   | 906    | 4  | Q13593  | Q13593 homo sapien            |
| 24     | 117.5  | 5.6   | 896    | 4  | Q13594  | Q13594 homo sapien            |
| 25     | 114    | 5.4   | 335    | 6  | P79203  | P79203 ovis aries             |

|    |       |     |       |    |        |              |
|----|-------|-----|-------|----|--------|--------------|
| 6  | 13.5  | 5.4 | 958   | 4  | 032920 | homo sapien  |
| 7  | 113.5 | 5.4 | 1165  | 4  | 092921 | homo sapien  |
| 28 | 113.5 | 5.4 | 896   | 4  | 092919 | homo sapien  |
| 29 | 110   | 5.2 | 6875  | 6  | 028733 | homo sapien  |
| 30 | 109.5 | 5.2 | 26926 | 4  | 010466 | homo sapien  |
| 31 | 107.5 | 5.1 | 710   | 13 | 057520 | xenopus lae  |
| 32 | 107   | 5.1 | 634   | 6  | 046600 | bos taurus   |
| 33 | 106   | 5.0 | 511   | 12 | 089000 | bos taurus   |
| 34 | 106   | 5.0 | 511   | 12 | 089664 | vesicular s  |
| 35 | 105.5 | 5.0 | 1835  | 5  | 061210 | caenorhabdi  |
| 36 | 102   | 4.8 | 229   | 6  | 027950 | bos indicus  |
| 37 | 101.5 | 4.8 | 233   | 4  | 000207 | homo sapien  |
| 38 | 101   | 4.8 | 800   | 11 | 063257 | rattus norv  |
| 39 | 101   | 4.8 | 511   | 12 | 088939 | vesicular s  |
| 40 | 100   | 4.8 | 229   | 6  | 028206 | bos taurus   |
| 41 | 100   | 4.8 | 817   | 13 | 007784 | gallus galli |
| 42 | 99.5  | 4.7 | 895   | 11 | 062960 | rattus norv  |
| 43 | 99    | 4.7 | 1093  | 5  | 070535 | rattus norv  |
| 44 | 98.5  | 4.7 | 2222  | 11 | 097394 | drosophila   |
| 45 | 98.5  | 4.7 | 2302  | 11 | 088488 | rattus norv  |

## ALIGNMENTS

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001 1
002 PRELIMINARY:
003 PRT: 383 AA.
004
005 088786:
006
007 01-NOV-1998 (TREMBLrel. 08, Created)
008
009 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
010
011 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
012
013 IL-13 RECEPTOR ALPHA 2.
014
015 Mus. musculus (Mouse).
016
017 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
018 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
019
020 [1]
021 SEQUENCE FROM N.A.
022
023 STRAIN=C3H/HEJ; TISSUE=THYMUS;
024
025 MEDLINE: 53391042;
026
027 DONALDSON D.D., WHITTEN M.J., FITZ L., NEBEN T.Y., FINNERTY H.,
028 HENDERSON S.D., O'HARA R.M. JR., BEIER D.R., TURNER K.J., WOOD C.R.,
029 COLLINS M.;
030
031 "The murine IL-13 receptor alpha 2: molecular cloning,
032 characterization, and comparison with murine IL-13 receptor alpha
033 1."
034
035 J. Immunol. 161:2317-2324(1998).
036
037 EMBL: U65747; AAC33240.1;
038
039 SEQUENCE 383 AA; 44483 MW; 5EAEE3E3 CRC32;
040
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Db 225 PELHISVENSIDIRKMNSTPGPIPPRCYVEIAREDDISWESATDKNDKLRANE 294  
 QY 301 TROLGVVRSKNVNYCDDGIMSEMSDKOCWEGEDLSKRTLLRFMLPFGFILLVFTVG 360  
 Db 295 SDDLCEFPKCKNINICADGIMSEMSSEECWEGCYGPDCKII-FTVPVCLFIFILLILLC 353  
 QY 361 LILKRPNTYPKM 372  
 Db 354 LIVEKEPEPTL 365

RESULT 2  
 Q14633 PRELIMINARY: PRT: 420 AA.  
 ID Q14633  
 AC Q14633;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, last annotation update)  
 DE INTERLEUKIN-5 RECEPTOR PRECURSOR.  
 GN HSIL5R.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 CC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PERIPHERAL BLOOD;  
 RX MEDLINE; 92121815.  
 RA MURATA Y., TAKAKI S., MIGITA M., KIKUCHI Y., TOMINAGA A., TAKATSU K.;  
 RT "Molecular cloning and expression of the human interleukin 5  
 receptor";  
 RL J. Exp. Med. 175:341-351(1992).  
 DR EMBL; X61176; CAA43483.1;  
 KW Signal.  
 FT CHAIN 1 20 POTENTIAL.  
 FT SIGNAL 21 420 INTERLEUKIN-5 RECEPTOR.  
 SO SEQUENCE 420 AA; 47670 MM; 247AB980 CRC32;

Query Match 14.8%; Score 311.5; DB 4; Length 420;  
 Best Local Similarity 26.9%; Pred. No. 7.9e-20;  
 Matches 100; Conservative 69; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIVNPPDFEYDPEYLGVLQOMOPPLSLDFKCEYVELEKRNISETKITIT 86  
 Db 25 DEKISLPPVNETIKYTG-LAQVLLQMKPNPDOQ-RVNNLEYQVKINAPKEDDEYETRT 82  
 QY 87 KNLHKDFDNLKGIKIHLLPMQCTNGSEVOSSNAETTYWISPOGIPETKYODMOCV 146  
 Db 83 ES---KCVTLHKGSASVRILO---NDHSLASSMASAEH-APPGSPGISVYNLCT 135  
 QY 147 -----YYNQYLL-CSMKPGIGVLLDTNLYF---WYEGDLHALQCVDYIKAD 191  
 Db 136 TTTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYRYSWTE-----ECQEYSKDT 189  
 QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSFTFQLONYKPLPYVLLFTTR 248  
 Db 190 LGRNACWFPPTFILSKGRDMLAVLVNGSSKHSARPDQFLALHAIDQINPPLNVTAEI 249  
 QY 249 ESSCEIRKMSIPLGPAPRCFDEYIEIREDDTLVTATVENETTYLTKTNETROLCFV 308  
 Db 250 EGT-RLSIQWKEPVSAPFIHCFDYEKIHNTNRNGYLQIEKMTNAPFISIIDLKSYDVOV 308  
 QY 309 RSKVNIYSDGIMSEMSDKOCWEGEDLSKRTLLRFMLPFGFILL-----VIFVTGL 362  
 Db 309 RAAVSSMCREAGIMSEMS-QPIYGVNDEHKP--LREW---FVIVMATICFILLIISLI 361  
 QY 363 LKRPNTYPKMIP 374  
 Db 362 CKICHLWIKLFP 373

RESULT 3  
 Q14631

ID Q14631 PRELIMINARY: PRT: 396 AA.  
 AC Q14631;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
 DT 01-NOV-1998 (TREMblrel. 08, last annotation update)  
 DE INTERLEUKIN-5 RECEPTOR TYPE 2 PRECURSOR.  
 GN HSIL5R2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 CC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PERIPHERAL BLOOD;  
 RX MEDLINE; 92121815.  
 RA MURATA Y., TAKAKI S., MIGITA M., KIKUCHI Y., TOMINAGA A., TAKATSU K.;  
 RT "Molecular cloning and expression of the human interleukin 5  
 receptor";  
 RL J. Exp. Med. 175:341-351(1992).  
 DR EMBL; X61177; CAA43484.1;  
 KW Signal.  
 FT CHAIN 1 20 POTENTIAL.  
 FT SIGNAL 21 396 INTERLEUKIN-5 RECEPTOR TYPE 2.  
 SO SEQUENCE 396 AA; 44998 MM; 85FBF684 CRC32;

Query Match 14.8%; Score 310.5; DB 4; Length 396;  
 Best Local Similarity 26.6%; Pred. No. 9e-20;  
 Matches 99; Conservative 70; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIVNPPDFEYDPEYLGVLQOMOPPLSLDFKCEYVELEKRNISETKITIT 86  
 Db 25 DEKISLPPVNETIKYTG-LAQVLLQMKPNPDOQ-RVNNLEYQVKINAPKEDDEYETRT 82  
 QY 87 KNLHKDFDNLKGIKIHLLPMQCTNGSEVOSSNAETTYWISPOGIPETKYODMOCV 146  
 Db 83 ES---KCVTLHKGSASVRILO---NDHSLASSMASAEH-APPGSPGISVYNLCT 135  
 QY 147 -----YYNQYLL-CSMKPGIGVLLDTNLYF---WYEGDLHALQCVDYIKAD 191  
 Db 136 TTTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYRYSWTE-----ECQEYSKDT 189  
 QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSFTFQLONYKPLPYVLLFTTR 248  
 Db 190 LGRNACWFPPTFILSKGRDMLAVLVNGSSKHSARPDQFLALHAIDQINPPLNVTAEI 249  
 QY 249 ESSCEIRKMSIPLGPAPRCFDEYIEIREDDTLVTATVENETTYLTKTNETROLCFV 308  
 Db 250 EGT-RLSIQWKEPVSAPFIHCFDYEKIHNTNRNGYLQIEKMTNAPFISIIDLKSYDVOV 308  
 QY 309 RSKVNIYSDGIMSEMSDKOCWEGEDLSKRTLLRFMLPFGFILL-----VIFVTGL 362  
 Db 309 RAAVSSMCREAGIMSEMS-QPIYGVNDEHKP--LREW---FVIVMATICFILLIISLI 361  
 QY 363 LKRPNTYPKMIP 374  
 Db 362 CKICHLWIKLFP 373

RESULT 4  
 Q920K4 PRELIMINARY: PRT: 415 AA.  
 AC Q920K4;  
 DT 01-MAY-1999 (TREMblrel. 10, Created)  
 DT 01-MAY-1999 (TREMblrel. 10, last sequence update)  
 DT 01-MAY-1999 (TREMblrel. 10, last annotation update)  
 DE INTERLEUKIN-5 RECEPTOR ALPHA PRECURSOR.  
 GN GPL-5RA.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 CC Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Norris T.E.;

"Cloning and Characterization of the Guinea Pig Interleukin-5 receptor alpha cDNA."

RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.

DR EMBL: U55125; AAD09361.1; -

KM Signal: Receptor.

FT SIGNAL 1 17 POTENTIAL.

FT CHAIN 18 415 INTERLEUKIN-5 RECEPTOR ALPHA.

SQ SEQUENCE 415 AA; 46913 MW; 99EBCB82 CRC32;

Query Match 14.2%; Score 298.5; DB 11; Length 415;

Best Local Similarity 26.5%; Pred. No. 1.1e-18;

Matches 103; Conservative 67; Mismatches 172; Indels 47; Gaps 19;

QY 6 LAIGLYTFLISTFGCTSSDTEIKVNPDPDEFYDGLYGLYLOMOPPLSLDHFKEC 65  
 DB 7 ILGAIETLQDTL-----PKKFLLPPIFTIKYTG-LAQVYLCEPENNQO-KNV 58  
 QY 66 TVEYELKYNIGSETWKIITKNLHYKDFDLNKGIEAKIHTLPWQCTNGSEVOSSMAE 125  
 DB 59 NLNHYVKINTPEEDYE--TRNTOSKCTTLHOGVSASVRLT-WH--GHSLLASSWVS 112  
 QY 126 TTYWISPGIPTKQDMDCV-----YNNQ-----YLCSMKRGISGLDNTNMLEF- 174  
 DB 113 AEH-KAPGSPGTSIVNLCTNTAASNTNLKSYEVSLHCTWLAGKDAPEDTQYFLYR 171  
 QY 174 --WYEGDLHALOCVDYIKAD--GONIGCRF--YLEASDYKDFYICVNGSSEKPIRSSY 227  
 DB 172 YGPWTE-----ECOEYSKDTLSRNTACFPFTFHSKRADLAHAVNGSSNHAITKPPD 225  
 QY 228 FTFOLONIYKPLPYVLTFTRESSCEIKLWSIPGLPIPARCFDYEIEI-REDDDTLVTA 286  
 DB 226 QLFQDAIDQPMPPMDVAETEGS-RLSIQWQKPVSAFPIHCFEYEVKICNTKDYQVER 284  
 QY 287 TYENETYLKTNEROLCFVVRSKVNIYCSDDGINSMSDQCMGEGELSKITLIR-FW 345  
 DB 285 TTNN--FVSTIDGVSKYSIOVRAASPHCRAMGLMSKMS-QPVYVKE--KKPIAGWPL 339  
 QY 346 LPFGFLLIVFVGTLLAKRPNTYPMIP 374  
 DB 340 ITLTAVLCFILLIFFFLCNLYHLMTKMP 368

RESULT 5  
 Q15469 PRELIMINARY; PRT: 333 AA.

AC 015469  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE SOLUBLE INTERLEUKIN-5 RECEPTOR PRECURSOR.  
 GN HSIL5R4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PERIPHERAL BLOOD;  
 RX MEDLINE: 92121815.  
 RA MURATA Y., TAKAKI S., MIGHTA M., KIKUCHI Y., TOMINAGA A., TAKATSU K.;  
 RT "Molecular cloning and expression of the human interleukin 5  
 receptor."  
 RL J. Exp. Med. 175:341-351(1992).  
 DR EMBL: X62156; CAA44081.1; -  
 KW SIGNAL  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 333 SOLUBLE INTERLEUKIN-5 RECEPTOR.  
 SQ SEQUENCE 333 AA; 37722 MW; E86A7792 CRC32;

Query Match 13.9%; Score 292; DB 4; Length 333;  
 Best Local Similarity 28.0%; Pred. No. 3.1e-18;  
 Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;

QY 27 TVEYELKYNIGSETWKIITKNLHYKDFDLNKGIEAKIHTLPWQCTNGSEVOSSMAE 86  
 DB 25 DEKISLDPPIFTIKYTG-LAQVYLCEPENNQO-RNVNLEYQKINAPKEDDETRET 82  
 QY 87 KNLHYKDFDLNKGIEAKIHTLPWQCTNGSEVOSSMAETTWISPGIPTKQDMDCV 146  
 DB 83 ES--KCVTLIKRGVSASVRLTQ--NDHSLASSMAEALH-APSPGTSIVNLCT 135  
 QY 147 -----YNNQYLL-CSMKRGISGLDNTNMLEF-----WYEGDLHALOCVDYIKAD 191  
 DB 136 TTTEDNTSRLSYOVSLHCTWLVTDAPEDTQYFLYRGSWTE-----ECOEYSKDT 189  
 QY 192 --GONIGCRF--YLEASDYKDFYICVNGSSEKPIRSSYFTFOLONIYKPLPYVLTFT 248  
 DB 190 LGRLNACMPREFELLSKGDMLAVLVNGSSKSAIRPDLFALHALDQINPLVTAEI 249  
 QY 249 ESSCEIKLWSIPGLPIPARCFDYEIEIREDDTLVTAVENTYTLKTNETROLCFVY 308  
 DB 250 EGT-RLSIQWQKPVSAFPIHCFEYEVKIHNTNGYLQIEKLTNAPISLIDLSKYDQV 308  
 QY 309 RSKVNIYCSDDGINSMS 326  
 DB 309 RAAVSSKREAGLMSWS 326

RESULT 6  
 Q05646 PRELIMINARY; PRT: 427 AA.  
 IC 05646  
 DT 01-MAY-1996 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)  
 DE INTERLEUKIN-5 RECEPTOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MORIMASA W., TERUMASA H.;  
 FT Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U81373; AAD03510.1; -  
 KW Receptor.  
 SQ SEQUENCE 427 AA; 48779 MW; BED0274E CRC32;

Query Match 13.9%; Score 291.5; DB 4; Length 427;  
 Best Local Similarity 26.8%; Pred. No. 4.7e-18;  
 Matches 98; Conservative 59; Mismatches 139; Indels 73; Gaps 20;

QY 53 WQPPSLDHFKECTVEY-----ELKYNIGSETWKIITKNLHYKDFDLNKGIEAKIHT 107  
 DB 52 WAPVVGAS--SNCSIMYSHFGDKODKIAPETRSI-----EVLNRIQLQVGS 100  
 QY 108 LIPWQ; TNGSEVOSSMAETTWIS-POGIPETKYQDMDCVYNNQYLLCSMKRGISGLV 165  
 DB 101 ----QOSTNESKPSILVKEC--ISPPEDPESAVTELCIHNLSYKMSVLPGRNTSP 154  
 QY 166 STYVNLFTYREGDLHALOCVDYIKADGONIGCRFPYLESD--YKDFYICVNGSSEKPI 223  
 DB 155 PTNYLLYVHRSLEKIHOC-ENIFREGOYFGCSFLTKKSDSFQHSQVIAWKDNAGRI 213  
 QY 224 RSYFTFOLONIYKPLPYVLTFTRESSCEIKLWSIPGLPIPARCFDYEIEIREDDT 281  
 DB 214 KPSFNIVPLTSKVPKDPPIKRLSFHND--DLVQWENPQN-FYSRCLFYEYVANSOT 269  
 QY 282 T-----LVTAVENTYTLKTNETROLCFVY-----RSKVNIYCSDDGI 321  
 DB 270 ETHNVEYVQACENPEERVENTS--CFWVPGLPDLNTVTRIVYTNKLCYEDDKL 326  
 QY 322 WSEMSDKQMBEDLSKITLRFNLPF-----GFLILVIVTGL--LLKRPNTY 370  
 DB 327 WSNWSQEM-----SIGKRNSTLYITMLLIVPVIVAGALIVLLYKRLKIIIFPIIDP 381

|                       |                                                                  |                                                              |              |
|-----------------------|------------------------------------------------------------------|--------------------------------------------------------------|--------------|
| OY                    | 371                                                              | -KMIPEEFCD                                                   | 379          |
|                       | :                                                                | :                                                            | :            |
| Dd                    | 382                                                              | GKIFKEMGD                                                    | 391          |
| <br>                  |                                                                  |                                                              |              |
| RESULT                | 7                                                                |                                                              |              |
| 097597                |                                                                  |                                                              |              |
| ID                    | 097597                                                           | PRELIMINARY:                                                 | PRT: 349 AA. |
| AC                    | 097597                                                           |                                                              |              |
| DT                    | 01-MAY-1999                                                      | (TREMBlrel. 10, Created)                                     |              |
| DT                    | 01-MAY-1999                                                      | (TREMBlrel. 10, Last sequence update)                        |              |
| DT                    | 01-MAY-1999                                                      | (TREMBlrel. 10, last annotation update)                      |              |
| DE                    | INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (FRAGMENT).      |                                                              |              |
| OS                    | Bos taurus (Bovine).                                             |                                                              |              |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;    |                                                              |              |
| OC                    | Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; |                                                              |              |
| OC                    | Bovinae; Bos.                                                    |                                                              |              |
| RN                    | (1)                                                              |                                                              |              |
| RP                    | SEQUENCE FROM N.A.                                               |                                                              |              |
| RA                    | TRIGONA W.L., HIRANO A., BROWN W.C., ESTES D.M.;                 |                                                              |              |
| RT                    | "Biological activities of interleukin-13 on bovine lymphocytes:  |                                                              |              |
| RT                    | implications for signaling through IL-13al."                     |                                                              |              |
| RL                    | Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.          |                                                              |              |
| DR                    | EMBL; AF074402; AAC98147.1; .                                    |                                                              |              |
| KM                    | Receptor.                                                        |                                                              |              |
| FT                    | NON_TER                                                          | 1                                                            | 1            |
| FT                    | NON_TER                                                          | 349                                                          | 349          |
| SQ                    | SEQUENCE                                                         | 349 AA; 39644 MW; AB48B972 CRC32;                            |              |
| <br>                  |                                                                  |                                                              |              |
| Query Match           |                                                                  | 12.6%; Score 264.5; DB 6; length 349;                        |              |
| Best Local Similarity |                                                                  | 24.4%; Pred No. 9.1e-16;                                     |              |
| Matches               |                                                                  | 83; Conservative 63; Mismatches 135; Indels 59; Gaps 16;     |              |
| OY                    | 53                                                               | WOPSLDHFKECVYEELKYRNIGSETWKITTKNLHYKDGFDLKKGIARHTLLPMQ       | 112          |
|                       | :                                                                | :                                                            | :            |
| Dd                    | 18                                                               | WNPPEGAS--PNCISLKY---FSHFNGKOKCKIAPEI-HRSKEVPINERICLOVGS---- | Q 67         |
| OY                    | 113                                                              | C-TNSEVOSSAETTYTWISPOGIEPTAKQDMDCYYNNQYLCSKPGSIGVLDTNW       | 171          |
|                       | :                                                                | :                                                            | :            |
| Dd                    | 68                                                               | CTNSEERSKSIIYEKCF-SPEGDDESATALOCIMHNLRYKMCWTLPNRNASPDPNYTL   | 126          |
| OY                    | 172                                                              | FYWEGSLDALOCVYIKRDGONICGRFYLEASD--YKDFCIYNSSSENPIRSSYPT      | 229          |
|                       | :                                                                | :                                                            | :            |
| Dd                    | 127                                                              | YTNHNSLGKIILCCENFYR-EGQHICSEFLTKVKOSSFEQHSQVAVRWGNACKISEPNT  | 185          |
| OY                    | 230                                                              | FOLQNIIVRPLRPVLYLTFFRESCEIKLKMSIPGLPIPAKPFYEIEIREDDTVLATVE   | 289          |
|                       | :                                                                | :                                                            | :            |
| Dd                    | 186                                                              | VPLTSGHVP-DPSHIKNLSFGNDLYOWTNPQN-FQSCLCYEVAVINSHA-----       | 236          |
| OY                    | 290                                                              | NETYILTAKTTNER-----QLCQVY-----RSKVITYI-SDDGIS                | 323          |
|                       | :                                                                | :                                                            | :            |
| Dd                    | 236                                                              | ETHDIIFYEEKAACONTREBNLEGTCIMPVGVLPDLINTVRIRYKTNKLCYEDDKLWS   | 294          |
| OY                    | 324                                                              | EWSDKQCWEGEDLSKKTLLRFWLPGFTILLIYFTGLL                        | 363          |
|                       | :                                                                | :                                                            | :            |
| Dd                    | 295                                                              | NWS-----QAMSIGOKANOTFIIT--TLILPIVYAAYAIV                     | 327          |
| <br>                  |                                                                  |                                                              |              |
| RESULT                | 8                                                                |                                                              |              |
| 064146                |                                                                  |                                                              |              |
| ID                    | 064146                                                           | PRELIMINARY:                                                 | PRT: 896 AA. |
| AC                    | 064146                                                           |                                                              |              |
| DT                    | 01-NOV-1996                                                      | (TREMBlrel. 01, Created)                                     |              |
| DT                    | 01-NOV-1996                                                      | (TREMBlrel. 01, Last sequence update)                        |              |
| DT                    | 01-NOV-1998                                                      | (TREMBlrel. 08, Last annotation update)                      |              |
| DE                    | INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).                  |                                                              |              |
| GN                    | RII-3RCBETA>                                                     |                                                              |              |
| OS                    | Rattus norvegicus (Rat).                                         |                                                              |              |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;    |                                                              |              |
| OC                    | Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.      |                                                              |              |
| RN                    | (1)                                                              |                                                              |              |

```

RD SEQUENCE FROM N.A.
RX MEDLINE: 95370942.
RA :PEPEL K., BUTTINI M., SAUTER A., GEBICKE-HAEFTER P.J.;
RT "Cloning of rat interleukin-3 receptor beta subunit from cultured
RL RT- microgilla and its mRNA expression in vivo";
RN J. Neurosci. 15:5800-5809(1995).
RE [2]
RC SEQUENCE FROM N.A.
RA STRAIN-WISTAR; TISSUE-BRAIN;
RL GEBICKE-HAEFTER P.J.;
DR EMBL; 579263; AB35068.1;
DR EMBL; AJ000555; CA040186.1;
PE PF00041; fn3; 2;
KM Signal.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 896 AA; 99504 MW; 8E7ED2CD CRC32;

Query Match 8.5%; Score 178; DB 11; Length 896;
Best Local Similarity 21.4%; Pred. No. 1.3e-07;
Matches 87; Conservative 65; Mismatches 167; Indels 88; Gaps 21;

OY 5 CLATGCL--YT FILSTFGCGSSSDTEIKV-----PPDFEYIDPGYGL 49
DB 94 CVPRCVLPYQFQSVSKEDYSLQPDRLSLHLYVLAHQVAPPKDISPSG-DHF 151
OY 50 YVOMQPL---SLDFKCTVEYEELKYNIGSETKITTLKHLKDGFDLKNKGEAKIH 106
DB 152 LKWSVPLGDQAVSLSSQKDIOFVAYKQL-QDSMD--ASLH-----TCLNWTLEPK 203
OY 107 TLTP-----WQCTNGSEVO---SSWAETTYWISPOGIPETKVOQMDCVYNNQYLL 154
DB 204 IFLPMSIYVARRAQALAPGSSLSGRPSGMSPEVHWDSPTE-DKARPNLQCFEFGDQSLN 262
OY 155 CSMKRGIGVLDNTNLTLYWHEGLDHALQCVDIYKADQONIGCRPFYELASRYKPFYICV 214
DB 263 CSMEWMTVWTDSVSGFLYSSSPKAGEKCKSPYVE-----LQASRYTYHOSL 311
OY 215 NGSSENKPIRSSYTFPOLO-----NIVKPLP-VYLFTRESSCEIKLWSIPL 262
DB 312 NVSD---FAHSQYIVSYKRLQCKGFISFNHIQNPPLTNLTKRDS---YSLHWETQK 365
OY 263 GPIPARCDYEIEIR-----EDDTLTATVAVENETYLKTINEROLCFVYRSKVNIYC 316
DB 366 MSYPIGHAFOYQYKKLDRMEDSKT-----ENLNAHNSMDLPQLEPGSYCARAVKTIIP 421
OY 317 SDDGWSWSDSKQCEGEDLSKTLIRWLPFGFLLIIVITYTGILL 363
DB 422 EYKGLMSMSNECTWT-TDWVWPLT--WI--VLIVFILPL 460

SEQUENCE 9
ID 057519 PRELIMINARY; PRT; 881 AA.
AC 057519;
DT 01-JUN-1998 (TREMBLrel. 06; Created)
DT 01-JUN-1998 (TREMBLrel. 06; Last sequence update)
DE 01-MAY-1999 (TREMBLrel. 10; Last annotation update)
DE GPI30P.
GN XGP130.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RR SEQUENCE FROM N.A.
RL CHEN J., GRACE A., CHIEN K.R.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF041845; AAC03531.1;
PE PF00041; fn3; 4;
KM FRAM; PF00041; fn3; 4;
SQ SEQUENCE 881 AA; 99003 MW; 647E152E CRC32;

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|                          |        |                    |            |             |
|--------------------------|--------|--------------------|------------|-------------|
| Query Match              | 8.28;  | Score 173.5;       | DB 13;     | Length 881; |
| Best Local Similarity    | 25.08; | Pred. No. 3,3e-07; |            |             |
| Matches 75; Conservative | 37;    | Mismatches 115;    | Indels 73; | Gaps 14     |

```
Oy 68 EYELKRYRNGSETWKTITTKNLIHYKDGDNLNKGEAKIHILLPWQCTNGSEVSQAETT 127
 :||: : ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 74 QYEILNQRTSSVTENLTLLN-----SPLTCNMASGHV-----ANTL 111
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QY 128 YMI -SPGQIRETKVDMDCCVYYNMQYLILCSMKRGIGVLDDTNYNLEY-W-YEGDLHALQC 184
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 112 YGIFFTLGLPPDKPITNLTCIYYNQDNLICTWDEGRPTNLPTNYILSHRMALFGANY---- 168

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Oy 185 VDYIKADGNIIGCRFPYLEASDVKDFPICVNGSSENKPIRSSYEFQLQNTYKKPLPEVY - 244
Db 168 -----CGRANNSCITHSPGFQFYIDTFQVEARNELGIOKSETLTI DPVNLYKPNPQLS 222

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Db 223 ELASSLEENALKIEWKNPIINAFNLKYNIRYRPVKTQDMEW-VREEDT-----ASHRDS 276

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D6 277 FTQDQLPNTVEVSIRC-----IHKDGHFWSMDSELKQYTPRAPPSRGPDIMWK 328
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|--------|--------|---------------------------|
| RESULT | 10     |                           |
| 0921A0 |        |                           |
| ID     | 0921A0 | PRELIMINARY; PRT; 890 AA. |

|    |                                                     |
|----|-----------------------------------------------------|
| DT | 01-MAY-1999 (TREMblrel. 10, Created)                |
| DT | 01-MAY-1999 (TREMblrel. 10, Last sequence update)   |
| DT | 01-MAY-1999 (TREMblrel. 10, Last annotation update) |

GN ILS.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

RN [1]  
RP SEQUENCE FROM N.A.  
RA LOGSDON N.J., GRAHAM A., SCOTT C.W.;  
RM "Evidence that the recombination beta chain is

RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U94688; AAC77520.1; -.  
 KW Receptor.  
 EC 800.11.06579.M3; FADBC130C.CBC32;  
 SC CONFIDENTIAL

|                       |       |                    |        |             |
|-----------------------|-------|--------------------|--------|-------------|
| Query Match           | 8.1%  | Score 170;         | DB 11; | Length 890; |
| Best Local Similarity | 23.8% | Pred. No. 6.8e-07; |        |             |

|         |     |                           |     |                                  |      |        |     |      |  |
|---------|-----|---------------------------|-----|----------------------------------|------|--------|-----|------|--|
| Matches | 88; | Conservative              | 53; | Mismatches                       | 144; | Indels | 84; | Gaps |  |
| QY      | 34  | PRODFEIVDPGYLGLYLQWPPSLDH | --- | FKCEVVEYELKRYRNGISETWTKIIITKNLIH | 90   |        |     |      |  |

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DB 136 PPDVQINISG--DQVLLIMSVALEGPHISWISQKULEEVLVIAKL-REFMESASI--LN 137
QY 91 YKDG-----FDLKNIGIAKIHITLPPWQCTNGSEVQ---SSWAETTYWISPGQIPETK 139

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140 VODMDCVYYNMQYLLCSWKPGLVLLTNYNLFXYWEGDLHALQ-CVDYIKADGQNT---196

**OY** 196 -GCRPYLEADYKDPYICVNGSSSENKPISRSTFTFOLQNIWKPLPPLYLTFTRESSCEI 250  
| : . : : | : ||| : : : | : : | : :

255 KLKWSIPLGPIPARCF-----DYEIEIREDDTLTVAIVENETYLK-----29

200 SEAM - A BENTONITE CLAY - A GOOD MEDIUM TO EMBROIDER UPON

[illegible]

|        |              |
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| RESULT | 11           |
| OJ0860 |              |
| ID     | 018880       |
|        | 00000        |
|        | PRELIMINARY; |
| PRT:   | 296 AA.      |

D1 01-JAN-1998 (TREMBLrel. 05, last sequence update)  
 D2 01-NOV-1998 (TREMBLrel. 08, last annotation update)  
 D3 PROLACTIN RECEPTOR SHORT FORM.  
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OC. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC. Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae;  
 OC. Bovinae; Bos.

PK MEDLINE; 97375450.  
 FS SCHUTLER L.A., NAGEL R.J., GAO J., HORSEMAN N.D., KESSLER M.A.;  
 RT "Prolactin receptor heterogeneity in bovine fetal and maternal  
 tissues".

```

LR EMBL; AF027403; AAB83999.1; -.
DR PFAM; PF00041; fn3; 2.
SQ
SEQUENCE 296 AA; 33854 MW; 8B40CCD8 CRC32;

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|                       |        |                    |        |                |
|-----------------------|--------|--------------------|--------|----------------|
| Query Match           | 7.8%   | Score 165;         | DB 6;  | Length 296;    |
| Best Local Similarity | 31.3%; | Pred. NO. 4.7e-07; |        |                |
| Matches               | 63;    | Conservative       | 24;    | Mismatches 96; |
|                       |        |                    | Indels | 18;            |
|                       |        |                    | Gaps   |                |

136 PETRYQDMDCVYYNMQYLCSKMPGIGVLLDTNYNLFYETEGLDHALQCVDIKADGONI 19

Oy 196 GCRPPYL<sup>3</sup>ASD<sup>1</sup>KDFICVNGSSSENKPIRSTYFTFQLO<sup>1</sup>NKYKPLPPYYLTFTR<sup>1</sup>ESSCEIK 25  
| | : : : | | : : | : | | | : : |  
Db 85 SCY<sup>3</sup>SK<sup>4</sup>TS<sup>1</sup>TWKMYITVNAINOMGISSDPLVHTYIIVEPEPANTLTLEIKHPEDRK 144  
| | : : : | | : : | : | | | : : |

Q7 256 ----LKHSIP-LGPIPARCF--DYEIETREODTLVATAVENET-YLUKTN-ETROLCF 30  
::: | : : : | ::| : : : |  
EJ 145 PYLWFKWSPPMTDVASGWFILOYILIRIKPEKAT-----DWETHFTLKQOLOKIFENLP 19

CY 307 VVRSKVATYCS-DDGIMSEWS 126  
: | | | | : | | | |  
D: 199 GGYTLVQIRCKPDHGIMSEWS 219

RESULT 13  
04/1/61

|    |                                                   |
|----|---------------------------------------------------|
| AC | 046561;                                           |
| D1 | 01-JUN-1993, (TREMBLrel, 06, Created)             |
| DE | 01-JUN-1998 (TREMBLrel, 06, Last sequence update) |

DE PROLACTIN RECEPTOR LONG FORM PRECURSOR.  
OS Ovis aries (Sheep).  
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:  
Eukaryota: Chordata: Craniata: Vertebrata: Mammalia: Placentalia: Bovidae: Bovinae: Caprinae: Ovis

CC Caprinae: Ovis.  
RE [1].  
REF SEQUENCE FROM N.A.  
RE REFERENCE: 0000140

RA ELEGANT C., BINART N., ORMANDY C., SCHULER L.A., KELLY P.A.,  
 FUYATE J.:  
 RA "3.05 and short forms of the ovine prolactin receptor: cDNA cloning  
 RT by genomic analysis reveal that the two forms arise by different

RT. In genomic analysis reveal that the two forms arise by different

RT alternative splicing mechanisms in ruminants and in rodents.";  
 RL J. Mol. Endocrinol. 19:109-120(1997).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RA BIGON C., DUANE J.,  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF041257; AAB96795.1;  
 DR PFAM; PF00041; fn3; 2.  
 KM Signal.  
 FT SIGNAL  
 FT CHAIN  
 SO SEQUENCE 581 AA; 65235 MW; 6792A7C7 CRC32; POTENTIAL.  
 PROLACTIN RECEPTOR LONG FORM.

Query Match 7.6%; Score 159; DB 6; Length 581;  
 Best Local Similarity 27.3%; Pred. No. 3.8e-06;  
 Matches 67; Conservative 25; Mismatches 103; Indels 50; Gaps 10;

OY 136 PETKQDMDCVYNNQYLCSKPKGIGVLLDTNINLFYWEGLDHALQCVDIKADGQNI 195  
 DB 27 PPEKRLIKRSPGKETFCWEPGADGGLPNTYLLTYRKEGELLHCEPDY-KTGGPN- 85  
 OY 196 GGRFFYLEASDVKDYICVNSSEKPIRSSYFTQLOINYPPLPVYLTFTRESSCEIK 255  
 DB 85 SCYFKKTSIMKMYVTVSAINQGISSDPLVYDVYIVPEPPVNLTLLEKPEDRK 144  
 OY 256 ---LKWSIP-LGPIPARCF--DYEIEIRDDTLVATVENEYTLKTNETROLCEVY 308  
 DB 145 PYLWKMSPTLTDVKSQGFISQIYELRLKPEKAT-----DMETHAPRLTDLKFNLYP 198  
 OY 309 RSK--VNITYCS-DGCIWSEMSDKOCWEGEDLSKTLRLFWLPGFILLIVITVGLLKK 365  
 DB 199 GOKYLVQIRCKPDHGWSEMS-----PESFIQI----- 227  
 OY 366 PNTYP 370  
 DB 227 PNDP 231

## RESULT 13

ID 046386 PRELIMINARY; PRT; 217 AA.  
 AC 046386.  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)  
 DE PROLACTIN RECEPTOR (FRAGMENT).  
 GN PRLR.  
 OS Mustela vison (American mink).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-TESTIS.  
 RA DOUGLAS D.A., SONG J.-H., HOUE A., MURPHY B.D.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF029294; AAB88899.1;  
 DR PFAM; PF00041; fn3; 1.  
 FT NON TER  
 FT NON TER  
 SO SEQUENCE 217 AA; 24850 MW; F77A3B9D CRC32;

Query Match 7.3%; Score 153; DB 6; Length 217;  
 Best Local Similarity 29.8%; Pred. No. 3.7e-06;  
 Matches 70; Conservative 26; Mismatches 87; Indels 52; Gaps 16;

OY 158 KPGIGVLLDTNINLFYWEGLDHALQCVDIKADQNIIGRFFYLEASDVKDYICVNV-- 216  
 DB 1 KPGEDGGLPTVYLLYHKEGFTTTCPCDYI-TSGPN-SCVFNKHTSIMWYIITINAT 58  
 OY 216 ---GSSEKPIRSSYFTQLOINYPPLPVYLTFTRESSCEIK-----LKWSIPL 262

DB 59 NEMGSSSDP---RYVT--LRYIVDPDPVNL-----SLEIKQPEDKTYLMIKW-YXP 106  
 OY 263 GPIPAR-----CFDYIEIRDDTLVATVENEYTLKTNETROLCEVNSK--VNICY 316  
 DB 107 TLVDYSGMLTQYELRLKPEKAT-----EETHFAGLQCFKILSIPOCKYLVQVC 160  
 OY 317 S-DGCIWSEMSDKOCWE-GEDLSKTLRLFWLPGFILLI-----VIFVTGILLR 364  
 DB 161 KPDHGFSEMSKRSIQIPNDISMKDTI-VMI---FVAVLSAVICLINVAVALK 211

## RESULT 14

ID 099665 PRELIMINARY; PRT; 862 AA.  
 AC 099665;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE IL-12 RECEPTOR BETA2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAVI N., WOU C.Y.,  
 RA GATELEY M.K., GUBLER U.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U64198; AAB36675.1;  
 DR PFAM; PF00041; fn3; 3.  
 SO SEQUENCE 862 AA; 97134 MW; 5F6AFBD5 CRC32;

Query Match 7.2%; Score 151; DB 4; Length 862;  
 Best Local Similarity 23.8%; Pred. No. 3.2e-05;  
 Matches 73; Conservative 42; Mismatches 108; Indels 84; Gaps 17;

OY 87 KNLHYKDFDLNKGIEAKIHILLP-----MQCTNGSEVQSSMAETTYWISPGIPE 137  
 DB 75 RINHHGHSINSQV-----TGLPLGTLFVCKLACINSDEIQGAEIFVGVAPE----- 126  
 OY 138 TKVDQDMCVYNNQ-YLLCSKPKGIGVLLDTNINL-----FYWEGDHALQCVDIK 189  
 DB 126 -QPNLSIQIGQEQVACTWGERGRDTHLYTEYTLQISGPNRLTWOK-----CKD-IY 177  
 OY 190 ADGONIGCRF-PYELASDYKDFICVN--GSSEKPIRSSYFTQLOINYPPLP--VYL 244  
 DB 178 CDYIDFGINLPESPESFTAKTAVANSLGSSSLP---STFT--LDIYVPLPPWDIRI 232  
 OY 245 TFRRESSCEIRLKW-----SIPLEGPIPARCFDYEIEIRDDTLVATVENEYTL 295  
 DB 233 KFOKASVSRCTLYWMBDEGLVLLNLRKRPSSRLMN-----MVNTYTKAKGRDL 281  
 OY 296 KTNETROLCEVNSKVNITYCSDDGCIWSEMSDK--QCWEGE-----DLK 338  
 DB 282 LDLPFYEFEPQISKLHLY--KGSWSDWESLRAQTPPEEPTGMIDWYMKRHIDYSR 338  
 OY 339 KTLRFW 345  
 DB 339 QOISLFW 345

## RESULT 15

ID 016354 PRELIMINARY; PRT; 206 AA.  
 AC 016354;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
 DE PROLACTIN RECEPTOR (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 RN [1]

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RP SEQUENCE FROM N.A.  
RX MEDLINE: 95286597.  
RA FUH G., WELLS J.A.;  
RT "Prolactin receptor antagonists that inhibit the growth of breast  
cancer cell lines."  
RL J. Biol. Chem. 270:13133-13137(1995).  
DR EMBL: S78505; AAB34470.1;  
PFAM: PF00041; fn3; 2.  
FT NON-TER  
SQ SEQUENCE 206 AA; 23950 MW; L7E57266 CRC32;

Query Match 7.2%; Score 151; DB 4; Length 206;  
Best Local Similarity 27.9%; Pred. No. 5, 2e-06;  
Matches 58; Conservative 26; Mismatches 94; Indels 30; Gaps 9;

QY 135 IPETKYQDMDCVYYNMQYLLCSNKPGLIGVLLDTNMLEFYWEGSLDHALOCVDYIKADGON 194  
DB 2 LPPGKPEIFKCRSPNKETETCWMRPGTDGGLPTNYSILYHREGETLMHECPDYI-TGGPN 60  
QY 195 IGCREFYLEASDYKDYICVNGSSSENKPIRSSYFTFQDNIVKPLRPVYLFTRESCEI 254  
DB 61 -SCHFGKQYTSMTYIMVNNATNMGSSFSDELVDYVYIVQDPPL-----ELAVEV 113  
QY 255 K-----LKWSIP-LGPDPARCFD--YEIREDDTLVATVENEYTLKTNET 301  
DB 114 KQPEDKKPYLMITWSPFTLIDLKTGMFTLIXEIRLKP-----KAEMEIHFAGQOTEF 167  
QY 302 ROLCFYVRSK--VNIYCS-DDGIWSEWS 326  
DB 168 KILSLHPGQKYLVQVRCRCKPDHGYWSAWS 195

Search completed: January 20, 2000, 06:37:46  
Job time: 1004 sec

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